

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 8, 2002, 08:57:07 ; Search time 24.95 Seconds

(without alignments)
1122.233 Million cell updates/sec

Title: US-09-579-383-3

Perfect score: 1982

Sequence: 1 NMFTVKYSFLVTCILCLLS.....SDNAAHNEQLAIEYEVSLH 378

Scoring table: BLOSUM62

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Database: A_Genseq_1101.*

1: /SID8/gcgdata/geneseq/AA1980.DAT.*
2: /SID8/gcgdata/geneseq/AA1981.DAT.*
3: /SID8/gcgdata/geneseq/AA1982.DAT.*
4: /SID8/gcgdata/geneseq/AA1983.DAT.*
5: /SID8/gcgdata/geneseq/AA1984.DAT.*
6: /SID8/gcgdata/geneseq/AA1985.DAT.*
7: /SID8/gcgdata/geneseq/AA1986.DAT.*
8: /SID8/gcgdata/geneseq/AA1987.DAT.*
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18: /SID8/gcgdata/geneseq/AA1997.DAT.*
19: /SID8/gcgdata/geneseq/AA1998.DAT.*
20: /SID8/gcgdata/geneseq/AA2000.DAT.*
21: /SID8/gcgdata/geneseq/AA2001.DAT.*
22: /SID8/gcgdata/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1982	100.0	378	22	AA1985
2	635	32.0	587	22	AA1986
3	135.5	6.8	298	20	AA1987
4	135.5	6.8	298	22	AA1988
5	134.5	6.8	509	21	AA1989
6	130	6.6	399	22	AA1990
7	128.5	6.5	361	18	AA1991
8	127.5	6.4	561	16	AA1992
9	127.5	6.4	561	17	AA1993
10	127.5	6.4	561	19	AA1994
11	126	6.4	555	21	AA1995

12	124.5	6.3	424	15	AA1996
13	122.5	6.2	490	21	AA1997
14	120.5	6.1	424	21	AA1998
15	120.5	6.1	424	21	AA1999
16	117.5	5.9	866	17	AA2000
17	117.5	5.9	866	21	AA2001
18	114	5.8	536	21	AA2002
19	113.5	5.7	561	15	AA2003
20	113	5.7	1215	21	AA2004
21	113	5.7	1215	22	AA2005
22	112.5	5.7	649	20	AA1989
23	112.5	5.7	668	20	AA1990
24	111	5.6	461	14	AA1991
25	111	5.6	461	20	AA1992
26	110.5	5.6	325	20	AA1993
27	110.5	5.6	349	20	AA1994
28	110.5	5.6	376	20	AA1995
29	110.5	5.6	376	22	AA1996
30	110.5	5.6	504	19	AA1997
31	108.5	5.5	1453	13	AA1998
32	107.5	5.4	541	19	AA1999
33	107	5.4	554	18	AA2000
34	107	5.4	554	21	AA2001
35	105	5.3	684	21	AA1993
36	104.5	5.3	1453	14	AA1998
37	104	5.2	851	21	AA1999
38	104	5.2	946	21	AA1999
39	103	5.2	452	22	AA2000
40	103	5.2	507	18	AA2001
41	103	5.2	1185	19	AA1998
42	102.5	5.2	377	22	AA1999
43	102.5	5.2	398	22	AA1999
44	102.5	5.2	787	22	AA1999
45	102	5.1	227	20	AA1999

ALIGNMENTS

RESULT 1
ID AAB49985 standard; Protein: 378 AA.
AC AAB49985;
DT 13-MAR-2001 (first entry)
XX
DE P. falciparum chitinase SEQ ID NO: 3.
XX
KW Malaria; mosquito; chitinase; fungal disease; parasitic disease;
XX veterinary disease; arthropod pest.
OS Plasmodium falciparum.
XX
FN W0200073488-A1.
XX
PD 07-DEC-2000.
XX
PE 26-MAY-2000; 2000WO-US14536.
XX
PR 28-MAY-1999; 99US-0136508.
PR 03-FEB-2000; 2000US-0180051.
XX
XX (TEXA) UNIV TEXAS SYSTEM.
PI Vinet J.M.
XX WPI: 2001-061553/07.
XX N-PSDB: AAC89668.
XX
XX New nucleic acid encoding a Plasmodium species chitinase is useful for
XX preventing transmission of malaria by mosquito feeding on subject that
XX may harbor Plasmodium species organisms

Trichoderma harzia
D. pteronyssius 98
T. harziaum strai
Amino acid sequenc
Soluble chitinase
Vibrio furnissii e
House dust mite (D
Bacterial chitinas
Superheat-resistan
Pyrococcus heat re
B. burgdorferi ant
B. burgdorferi ant
B. burgdorferi. Sta
B. epidermis readi
B. burgdorferi ant
Streptomyces albid
Amino acid sequenc
Vibrio harveyi end
CCV-C54 spike prot
Entodinium caudatu
Manduca sexta larv
Manduca sexta gut
L. mycophilus chit
E2 protein of Cani
V. furnissii extra
Plasmodium falcipa
S. aureus DNA UDP-
H. pylori chaparon
H. pylori GHP0 123
Disease treatment
Disease treatment
Glycerol dehydrata
Enterococcus faeca

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XX Claim 29; Page 124-125; 137pp; English.
PS
XX
CC The present invention provides the protein and coding sequences of the
CC Plasmodium falciparum and P. gallinaceum chitinase enzymes. These
CC organisms are the cause of malaria in humans. The sequences are useful
CC in the prevention and treatment of malaria, fungal diseases, parasitic
CC diseases and veterinary diseases, in preventing the transmission of
CC malaria and in the control of arthropod pests in agriculture.
XX
SQ Sequence 378 AA;

Query Match 100.0%; Score 1982; DB 22; Length 378;
Best Local Similarity 100.0%; Pred. No. 2.1e-177;
Matches 378; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MNFTVYKSYFLVYICLLCCLSTVSYVIEGHARARQESRKNRREITKTKESGKIIOGYR 60
DB 1 mntfvysflvliccllststsvsieghararqesrknprrlktikesgkllggyyp 60
OY 61 SWVSYYHNKLDLPNLNVVMSFAKMDLSYDSIESIVSGPLTFKSLIGLEYIGLNEYFND 120
DB 61 swvsyyhnkldlnpnlvvmsfakmdlsydsiesivsgplltfksllgleyiglneyfnd 120
OY 121 AMNLRRARPDITMLSLGGETYHPSSFDSALNVEKIANLVDELGFDDIDVDYEPNGSFD 180
DB 121 amnlrrarpditmlslggetyhpssfdsalnvekianlvdelgfdgidvdyepngsfd 180
OY 181 GUNDRKKAFFQVQYVTKRKYMCDDKILISQSSNGALSCIGFNDPKKICMDDEAPYNSK 240
DB 181 gundrkkaaffvqvvtkrkymcddkilsisqssngalscigfndppkkicmddeapynsk 240
OY 241 YNNKPPVKKELRAAOMASGAIYLMNNLKMDIMVFOVFNTYNTSDSTVMKELDSY 300
DB 241 ynnkppvkkelraaomasgaitylmnnlkdmdimvfovfntyntsdstvmkeldsy 300
OY 301 AYYGKKYDVIYIIGFTLMPESTPFNPNDKMLVNSIGDFVTENKLNKRADGFGMLSSD 360
DB 301 ayygkkdydviyigftlmpestpfpnpndkmlvnsigdfvtenklnkradgfgmlssd 360
OY 361 NAAHNQOLAIEYFVESLH 378
DB 361 naahneqlaieyiveslh 378

RESULT 2
AAB49986
ID AAB49986 standard; Protein; 587 AA.
XX
AC AAB49986;
XX
DT 13-MAR-2001 (first entry)
XX
DE P. gallinaceum chitinase SEQ ID NO: 4.
XX
KW Malaria; mosquito; chitinase; fungal disease; parasitic disease;
KW veterinary disease; arthropod pest.
XX
OS Plasmodium gallinaceum.
XX
PN WO200073488-A1.
XX
PD 07-DEC-2000.
XX
PE 26-MAY-2000; 2000MO-US14536.
XX
PR 28-MAY-1999; 99US-0136508.
XX
PR 03-FEB-2000; 2000US-0180051.
XX
PA (TEXA ) UNIV TEXAS SYSTEM.
XX
PI Vinetz JM;
```

```
XX WPI: 2001-061553/07.
DR N-PSDB; AAC09669.
XX
PT New nucleic acid encoding a Plasmodium species chitinase is useful for
PT preventing transmission of malaria by mosquito feeding on subject that
PT may harbor Plasmodium species organisms
XX
XX Claim 29; Page 125-127; 137pp; English.
XX
SQ Sequence 587 AA;

Query Match 32.0%; Score 635; DB 22; Length 587;
Best Local Similarity 37.4%; Pred. No. 7.9e-51;
Matches 129; Conservative 82; Mismatches 126; Indels 8; Gaps 5;

OY 37 RKNPREIITKTKESGKIIOGYPSWVSYNHNLK---DLNPNLVVMSFAKMDLSTDSI 93
DB 37 rknpreiitktkesgkllggypswvsynhnlk---dlnpnlvvmsfakmdlstdsi 93
OY 89 RKSPrqllleeykkrrkggllaggygswsgdgrakhmidsnpwsllyafatimlydvs 148
DB 89 rksprqllleeykkrrkggllaggygswsgdgrakhmidsnpwsllyafatimlydvs 148
OY 94 ESTVSGPLFLFSLIGLEYIGLNEYFNDAMNLRARPDITMLSLGGETYHPSSFDSALN 153
DB 94 estvsgplflfsligleyiglneyfndamnrrarpditmlslggetyhpssfdsaln 153
OY 149 rpfngqrflrlrkhlleyetygmnlneirtrfkvrpavilllsgyetymldekeidy 207
DB 149 rpfngqrflrlrkhlleyetygmnlneirtrfkvrpavilllsgyetymldekeidy 207
OY 154 VEKIANLVDELGFDDIDVDYEPNGSFDGLNDRKADFFQVYVTKRKYMCDDKILISQSS 213
DB 154 vekianlvdelgfdgidvdyepngsfdglndrkadffqvvtkrkymcddkilsisqs 213
OY 208 vdkllkivndldvgldvephgkfylnelnfsnyyiklilnlrtklpeklisigs 267
DB 208 vdkllkivndldvgldvephgkfylnelnfsnyyiklilnlrtklpeklisigs 267
OY 214 SNGALSCIGFNDPKKICMDDEAPYNSKYFNKP-DYKKEILRAAOMASGAIYLMNNLK 272
DB 214 sngalscigfndppkkicmddeapynskfnpkpykkelraaomasgaitylmnnlk 272
OY 268 snaaliscv--sgvasfckdeespyntkflseqletnklraaamsagflnflntake 325
DB 268 snaaliscv--sgvasfckdeespyntkflseqletnklraaamsagflnflntake 325
OY 273 MIDWFOVFNTYNTSDSTVMKELDSYAYYGGKYDVIYIIGFTLMPESTPFNPNDKMLV 332
DB 273 midwfovfntyntsdstvmkeldsyayyggkydviyigftlmpestpfpnpndkmlv 332
OY 326 kidlvifqlytn-lettrpdlmwamyishlyfglykylntllilgfslenrgyfspenkell 384
DB 326 kidlvifqlytn-lettrpdlmwamyishlyfglykylntllilgfslenrgyfspenkell 384
OY 333 KSIDGFVTENKLNKRADGFGMLSSDNAHNEQOLAIEYFVESL 377
DB 333 ksidgfvtenklnkradgfgmlssdnaahneqolaieyvesl 377
OY 385 elvgktihdkngnnrnradgigivhlfnkqglprgsfdvdfilnli 429
DB 385 elvgktihdkngnnrnradgigivhlfnkqglprgsfdvdfilnli 429

RESULT 3
AAY33721
ID AAY33721 standard; Protein; 298 AA.
XX
AC AAY33721;
XX
DT 09-NOV-1999 (first entry)
XX
DE Streptomyces albidoflavus mature chitobiosidase.
XX
KW Chitin; chitinolytic enzyme; insect; fungus; resistance;
KW transgenic plant; insecticide; fungicide.
XX
OS Streptomyces albidoflavus.
XX
PN WO9942594-A1.
XX
PD 26-AUG-1999.
XX
PR 12-FEB-1999; 99MO-US03176.
XX
PR 18-FEB-1998; 98US-0025691.
XX
PA (CORR ) CORNELL RES FOUND INC.
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XX Broadway RM, Harman GE;
 PI
 XX WPI: 1999-527480/44.
 DR N-PSDB; AA206824.
 XX
 PT New nucleic acid encoding chitinolytic enzyme active under alkaline
 PT conditions, used to generate plants resistant to insects and fungi
 PT and to produce recombinant enzyme
 XX
 PS Claim 6; Page 10-11; 90pp; English.
 XX
 CC This sequence represents Streptomyces albidoflavus chitinobiosidase.
 CC Chitinobiosidase hydrolyses chitin, an insoluble linear
 CC beta-1,4-linked polymer of N-acetyl-beta-D-glucosamine found in all
 CC arthropods, yeast, most fungi, and some stages of nematodes. There are
 CC three types of chitinolytic enzyme activity: glucosaminidase, which
 CC cleaves monomeric units from the terminal end of chitin; chitinobiosidase,
 CC which cleaves dimeric units from the terminal ends; and
 CC endochitinase, which randomly cleaves the chitin molecule internally.
 CC Chitinobiosidase and endochitinase (AAV3722) from S. albidoflavus are
 CC active under alkaline conditions. This makes them particularly effective
 CC in controlling insects, as these enzymes can be ingested by insects and
 CC can then attack them by degrading their chitin-containing, alkaline
 CC digestive tracts. These chitinolytic enzymes can be applied directly to a
 CC plant to act as an insecticide or fungicide, or non-pathogenic bacteria
 CC transformed with the DNA encoding either or both enzymes can be applied
 CC to a plant. Alternatively, transgenic plants can be produced which
 CC express either or both enzymes in some or all of their tissues. A wide
 CC variety of commercially important crops could benefit from use of these
 CC enzymes e.g. sugar cane, potato, cotton and coffee.
 XX
 SQ Sequence 298 AA;
 Query Match 6.8%; Score 135.5; DB 20; Length 298;
 Best Local Similarity 21.7%; Pred. No. 0.0002;
 Matches 55; Conservative 50; Mismatches 76; Indels 73; Gaps 12;
 QY 55 IQGYPSWVSYNH-----NLKDLNPNLVHMSFAKMDLSYDSISIVGSPLLFKSLGL 109
 Db 10 vtyg---wqnfngatvgtladvpdaydlavsfadatanagel-----tftl 54
 QY 110 EYIGLNEVFNDAMNLRKARPDII-----MLSLGGETYPPSSRDSALNVEKIAN-- 159
 Db 55 dsvglggytde-----qfradlaakqadgksvllsvggekavavnds--saqrfadst 107
 QY 160 --LVDELGFDIDVDYEPNGSFDGLNDEKADPFQVYTKLREVMCDKLTISISQSSNGA 217
 Db 108 yalmeeygfdgvdldle-----ngln-----stymtealtklhekagdgdlvltmapqt--- 155
 QY 218 LSCIGFNDPKKICMDEAPYNSKYFNKPDVKKELLRA-----AQMASAGCAIYLMNN 269
 Db 156 -----ldmspsen-eyfkltavtkcfdltavmgyngsgmlgdcggyayagt 201
 QY 270 LKDMIDMVFVQTFN 283
 Db 202 vdfiltalaciqlen 215
 RESULT 4
 AAG63552 standard; Protein; 298 AA.
 ID AAG63552;
 AC AAG63552;
 XX
 DT 15-OCN-2001 (first entry)
 XX
 DE Amino acid sequence of a chitinobiosidase polypeptide.
 XX
 KW Chitinobiosidase; chitinolytic enzyme; early flowering.
 XX
 OS Streptomyces albidoflavus.

XX WO200146387-A1.
 PN
 XX 28-JUN-2001.
 PD
 XX
 XX 22-DEC-2000; 2000WO-US35238.
 PE
 XX 23-DEC-1999; 99US-0172003.
 PR
 XX (COR) CORNELL RES FOUND INC.
 PA
 XX Broadway RM, Gongora CE;
 PI
 XX WPI: 2001-496661/54.
 DR N-PSDB; AAH74537.
 XX
 PT Promoting early flowering, yield in plants and reducing plant size,
 PT involves growing transgenic plant or plant seed transformed with DNA
 PT molecule encoding chitinolytic enzyme, or applying the enzyme to the
 PT plant
 XX
 PS Claim 7; Page 10-11; 87pp; English.
 XX
 CC The present sequence represents a chitinobiosidase polypeptide. The
 CC polypeptide has a molecular mass of 34 kD and an isoelectric point
 CC of less than 3. The polypeptide is a chitinolytic enzyme. The
 CC chitinolytic polynucleotide is used to produce transgenic early
 CC flowering plants. The chitinolytic polynucleotides and polypeptides
 CC are useful for promoting early flowering in plants, promoting yield
 CC from plants and reducing plant size.
 XX
 SQ Sequence 298 AA;
 Query Match 6.8%; Score 135.5; DB 22; Length 298;
 Best Local Similarity 21.7%; Pred. No. 0.0002;
 Matches 55; Conservative 50; Mismatches 76; Indels 73; Gaps 12;
 QY 55 IQGYPSWVSYNH-----NLKDLNPNLVHMSFAKMDLSYDSISIVGSPLLFKSLGL 109
 Db 10 vtyg---wqnfngatvgtladvpdaydlavsfadatanagel-----tftl 54
 QY 110 EYIGLNEVFNDAMNLRKARPDII-----MLSLGGETYPPSSRDSALNVEKIAN-- 159
 Db 55 dsvglggytde-----qfradlaakqadgksvllsvggekavavnds--saqrfadst 107
 QY 160 --LVDELGFDIDVDYEPNGSFDGLNDEKADPFQVYTKLREVMCDKLTISISQSSNGA 217
 Db 108 yalmeeygfdgvdldle-----ngln-----stymtealtklhekagdgdlvltmapqt--- 155
 QY 218 LSCIGFNDPKKICMDEAPYNSKYFNKPDVKKELLRA-----AQMASAGCAIYLMNN 269
 Db 156 -----ldmspsen-eyfkltavtkcfdltavmgyngsgmlgdcggyayagt 201
 QY 270 LKDMIDMVFVQTFN 283
 Db 202 vdfiltalaciqlen 215
 RESULT 5
 AAY52533 standard; Protein; 509 AA.
 ID AAY52533;
 AC AAY52533;
 XX
 DT 22-FEB-2000 (first entry)
 XX
 DE D. pteronyssius 98 kD mite allergen protein (map) PDerp98-509.
 XX
 KW Mite allergen protein; map; high molecular weight; HMW-map; allergy;
 KW house dust mite; IGE; immunoglobulin E; allergen; mapB;
 KW hypersensitivity reaction; therapy; treatment; diagnosis; human; feline;
 KW canine; veterinary; antibody; vaccine; immunisation.

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XX OS Dermaphagoides pteronyssius.
XX FH Key Location/Qualifiers
XX FT Peptide 1..19
XX FT Protein /note="Signal peptide"
XX FT Protein /note="Mature PDerp98-509"
XX PN WO9954349-A2.
XX PD 28-OCT-1999.
XX PF 16-APR-1999; 99MO-US08524.
XX PR 17-APR-1998; 98US-0062013.
XX PR 13-MAY-1998; 98US-0085295.
XX PR 02-SEP-1998; 98US-0098909.
XX PA (HESK-) HESKA CORP.
XX PI McCall CA, Hunter SW, Weber ER;
XX DR WPI: 2000-052700/04.
XX DR N-PsDB: AA238585, AA238586, AA238587, AA238588.
XX PT Novel high molecular weight Dermatophagoides nucleic acid polypeptides
XX PT used to modify an animals' hypersensitivity to mite allergens
XX PS Claim 3; Page 134-136; 154pp: English.
XX CC This sequence represents Dermatophagoides pteronyssius mite allergen
XX CC protein (map). Pderp98-509. Pderp98-509 has a molecular weight of 98 kD,
XX CC comprising 509 amino acids, and has a high degree of homology with the
XX CC D. farinae 98 kD allergen, mapB (AAV52523). Nucleic acid molecules
XX CC encoding Pderp98-509 were isolated from a D. pteronyssius cDNA library
XX CC by hybridisation with a probe encoding the D. farinae high molecular
XX CC weight map (Hmw-map) composition. Mite allergenic proteins and
XX CC peptides, and nucleic acids encoding them, may be used in therapeutic
XX CC compositions to modify an animal's hypersensitivity reaction to mite
XX CC allergens. Animals that may be treated include mammals and birds,
XX CC especially felines, canines, equines, humans, other pets, and work or
XX CC domestic animals. The proteins or fragments may also be used to
XX CC diagnose allergies via a skin test. The proteins and peptides can also
XX CC be used to raise antibodies, which have a variety of potential
XX CC uses. For example, they can be used as vaccines to passively immunise
XX CC animals against dust mite hypersensitivity, as positive controls in
XX CC test kits and as tools to recover desired dust mite allergens from a
XX CC mixture of proteins.
XX SQ Sequence 509 AA:

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Query Match 6.8%; Score 134.5; DB 21; Length 509;
Best Local Similarity 22.1%; Pred. No. 0.00054;
Matches 83; Conservative 51; Mismatches 128; Indels 113; Gaps 20;

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OY 5 VVSYFLVLCCLSTVYSVIEGHRARPESSRRNPRIITKTESGKGIIGYPPSWMS 64
DB 1 mktfalciwaciglmnatkrch-----nysknpmriv-----cyvgtwsv 44
OY 65 YN-----HNKLDLPNPNLVYHM--SFAKMDLSYDSIESIVGSPLLFKSLIGLEYIGLNEYF 118
DB 45 ykhvdpqytiedidp-fkcthlmygfaideykyltg--vtdpfdqddhnswekhngy-erf 100
OY 119 NGAMNRRKARPDIIIMLSLGG-----ETVHPSFDSALNA-----VEKIANLVDEIGDP 167
DB 101 n---nlrlknpeitmtisigwtyegsekys-----dmaapntyrgqfvgsvldfigeykfd 153
OY 168 GIDVDYEPNGSGFDGLNDKEKADPFVVOYVTKLREYMCDDKLISQSNGALSCIGFNDPK 227
DB 154 gldldweygsrslg-npkldkqnyltivrelke-----afepfgy-----192

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OY 228 KICMDDEAPYNSKYFNKPDYKKEILLRAAQMASAG-----GAIYLMNNIKMDIDWVYOTFN 283
DB 193 -----lltaa--vspgkdkidvayelkelnglfdmnmvntld 227
OY 284 YTNSTDSIV-----MKELYDSYAVYGGKY--DYVILMGFT-----LMFPSTPFN 325
DB 228 yhgwenvfghmaplrykprdetdelhcyfnvnylmhylimngatrdklmgvpyfgyraws 287
OY 326 PNDKMLVKSIGDFVK 340
DB 288 ledrskvk-lgdgpk 301

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RESULT 6
AAU00962
ID AAU00962 standard; Protein: 399 AA.
AC AAU00962;
XX 12-SEP-2001 (first entry)
DT F. venenatum endochitinase polypeptide.
XX DE
XX XX Glucanase; endochitinase; exochitinase; cell-wall degradation; fungus;
XX KW transgenic plant; plant pathogen; bacteria; seafood waste; shell;
XX KW chitin; chemical modification; glucan.
XX OS Fusarium venenatum.
XX PN WO200116353-A1.
XX PD 08-MAR-2001.
XX PF 30-AUG-2000; 2000MO-US23802.
XX PR 30-AUG-1999; 99US-0151582.
XX PR 11-AUG-2000; 2000US-0224946.
XX PR 28-AUG-2000; 2000US-0649747.
XX PA (NOVO ) NOVO NORDISK BIOTECH INC.
XX PA (USDA ) US SEC OF AGRIC.
XX PI Okubara PA, Blechl AE, Hohn TM, Berka RM;
XX DR WPI: 2001-218524/22.
XX DR N-PsDB: AAS00796, AAS00800.
XX PT Fusarium nucleic acids encoding polypeptides having glucanase,
XX PT endochitinase or exochitinase activity, useful for producing transgenic
XX PT plants which are resistant to plant pathogens, particularly Fusarium
XX PT species -
XX PS Claim 13; Page 167-168; 216pp: English.
XX CC The sequence represents the Fusarium fungal enzyme, endochitinase.
XX CC Glucanase, endochitinase and exochitinase are polypeptides with cell-wall
XX CC degrading activity, derived from Fusarium fungal genes. The associated
XX CC nucleic acids can be used to produce transgenic plants which are
XX CC resistant to plant pathogens, particularly Fusarium species. They can
XX CC also be used to isolate homologous genes from fungi to obtain genes which
XX CC protect host cells, including fungi, bacteria and plants against related
XX CC fungal pathogens. The polypeptides, especially chitinases and glucanases,
XX CC are useful for degrading seafood waste, such as shells that contain
XX CC chitin, or for chemical modification of chitin or glucan.
XX SQ Sequence 399 AA:

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Query Match 6.8%; Score 130; DB 22; Length 399;
Best Local Similarity 22.4%; Pred. No. 0.001;
Matches 73; Conservative 51; Mismatches 112; Indels 90; Gaps 16;

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OY 58 YVPSWVSY--NHNKLDLPNPNLVYHMSFAKMDLSYDSIESIVGSPLLFKSLIGLEYIGLN 115

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Db      13 yfwnaiyatkhhpqdl-pvenlthily-----sfanirsdsgvnhltdswadtdlhwg 66
QY      116 EYENDL-----MNLKRRAR-PDITMLSLGGETYH-----PSSFDLSALNAVEK-IA 158
Db      67 dswndvgtlnlygmckgnllkrrnrlkvlslgswtfssnfkgpatpggrdtfakscv 126
QY      159 NLVDELGFDCIDVDYE-PNGSFDGLNDKEADFFVOYVTKLREYMCDDKLISISQSSNGA 217
Db      127 dlknltgfdgididweyp-----qdanearyvellgavrhnm-dayaqtlisq----- 173
QY      218 LSGIGFNDPKKICMDDEAPYNSKYFNKPDKKELLRRAQAASAGAIYLMNNLKMDIMV 277
Db      174 -----pyhfeltvaacpagatnftqklidr-----gmdqyldfw 205
QY      278 FVOYFNTNSTDSTV--MKELDYSAVYGGKRYVILMGFTLMEPSYFPNPKMLVKSII 335
Db      206 nlmaydyagwdqtaghqnalyps-----hdnpy-----stpfacts-----aal 244
QY      336 GDRVKTENKLNKRADGFGMLSSSDN 361
Db      245 dlyvrsqvmpekivlgmplygrafen 270

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RESULT 7

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AAW29178
ID      AAW29178 standard; Protein; 561 AA.
XX
AC      AAW29178;
XX
DT      06-MAR-1998 (first entry)
XX
DE      S. marcescens chitinase A.
XX
KW      Serratia marcescens; chitinase A; transgenic plant; cold resistant;
KM      reducing sugar; increased level.
XX
OS      Serratia marcescens.
XX
PN      US5633450-A.
XX
PD      27-MAY-1997.
XX
PE      01-DEC-1995; 950S-0566347.
XX
PR      19-DEC-1994; 94US-0358901.
PR      26-MAR-1984; 84US-0593691.
PR      18-JUL-1986; 86US-0888033.
PR      09-JUL-1990; 90US-0550253.
PR      14-AUG-1992; 92US-0930970.
PR      01-DEC-1995; 95US-0566347.
XX
PA      (DNAP ) DNA PLANT TECHNOLOGY CORP.
XX
PI      Jones JDC, Suslow TV;
XX
DR      WPI; 1997-297423/27.
XX
N-PSDB; AAT86836.
XX
PT      Transgenic plants expressing chitinase - with increased cold
PT      resistance or sugar content
XX
PS      Example 3; Columns 25-30; 25pp; English.
XX
CC      This sequence represents the Serratia marcescens chitinase A.
CC      information from the DNA coding it (AAT86836) was used in the creation of
CC      constructs which led to the expression of the bacterial chitinase gene in
CC      plant cells. Plants which have been transformed with chitinase-encoding
CC      DNA so that they express active chitinase are resistant to cold damage or
CC      have enhanced reducing sugar levels. The plants, especially tomato
CC      plants, have improved frost resistance or produce sweeter fruits.
XX
SQ      Sequence 561 AA.

```

Query Match 6.5%; Score 128.5; DB 18; Length 561;
 Best Local Similarity 23.2%; Pred. No. 0.0023;
 Matches 83; Conservative 44; Mismatches 114; Indels 117; Gaps 21;

```

QY      2 NFTY-----KISFLYICLLC-----CLSTIYSVT-----EGHARRGESKKNP-REIITKFK 48
Db      99 nfkvnkgqrgymqy--alcnadgctasdateivvadtdgrhlpp---lkeplleknpkyk 153
QY      49 ESGKGIIOGYVPWSVYNHNK-LDNPMLNVHMSFAKMDLS-----YDSIESIYGS-PL 101
Db      154 gnsqkvvgsyfwewgyvgrnftvdklpeqntlhllygfipicgnglndstikelegstqa 213
QY      102 LFKSLIGLEYIGLNEY-----FNDANNLRKRPDIIMLSLG 138
Db      214 lqrcsgredtklshdpfaalqkqkvtaoddpykgnfglnalkeghpdlklppisg 273
QY      139 GETYHPSSF-----DSALNAVEKIANLVDELGFDCIDVDYE---PNGSFDGLNDKEK 187
Db      274 gwltstdpffimgdkvkdrifgsvkef--lqtwkffidgvdldwefpgqkganpnlgsppd 331
QY      188 ADFVVOYVTKLREYMCDDKLISISQSSNGALSCIGFNDPKKICMDDEAPYNSKYFNKPDPV 247
Db      332 getyvlmkelraml--dql-----saetgrky----- 357
QY      248 KKELLRAAQAASAGAIYLMNNLKMDIMVFOYFNT--NSTDSTVMEKYDYSAAYYG 304
Db      358 --eltsa---lsag-----kdkldkv---aynvagasmhllm---sydfyg 394

```

RESULT 8

```

AAR64823
ID      AAR64823 standard; Protein; 561 AA.
XX
AC      AAR64823;
XX
DT      23-JUL-1995 (first entry)
XX
DE      Chitinase A.
XX
KW      Chitinase A; protein secretion; biological control agent;
KM      transgenic plant; chitin; plant pathogen; nematode; fungus;
KW      crop protection; pchir1251.
XX
OS      Serratia marcescens QMB1466.
XX
FH      Key Location/Qualifiers
FT      Peptide 1..23 /label= sig_peptide
XX
PN      US5374540-A.
XX
PD      20-DEC-1994.
XX
PE      26-MAR-1984; 84US-0593691.
XX
PR      26-MAR-1984; 84US-0593691.
PR      18-JUL-1986; 86US-0888033.
PR      09-JUL-1990; 90US-0550253.
XX
PA      (DNAP ) DNA PLANT TECHNOLOGY CORP.
XX
PI      Jones JDC, Suslow T;
XX
DR      WPI; 1995-035648/05.
XX
N-PSDB; AAQ76290.
XX
PT      Plant cell contg. signal sequence of chitinase A gene - for
PT      secretion of foreign polypeptide, esp. chitinase A for protection
PT      against pathogenic fungi and nematodes.
XX
PS      Disclosure; Fig. 1A-1C; 20pp; English.

```

xx Serratia marcescens QMB1466 genomic DNA was partially digested,
 CC ligated into vector pLAFRI, packaged into lambda phage particles,
 CC and used to transfect *Escherichia coli* DH1 (ATCC 33849) cells.
 CC Plating on chitin medium was used to screen for chitinase activity.
 CC Clone C12 (ATCC 67152) was isolated. Its sequence is given in
 CC AA076290, and the deduced protein sequence in AAR64823.

xx Sequence 561 AA:

Query Match 6.4%; Score 127.5; DB 16; Length 561;
 Best Local Similarity 23.2%; Pred. No. 0.0028;
 Matches 83; Conservative 44; Mismatches 114; Indels 117; Gaps 21;

QY 2 NFTV---KYSFLVYICLLC---CLSTYVSV---EGHRARPGESRKNP-REIITFK 48
 Db 99 ntkvknkgrygmqv--alcnadgctasdateivvadtdgshlpp---lkeplleknpkyk 153
 QY 49 ESGKGIIQGYPSWVSYNHNLK-DLNPNLNVHMSFAKMDLS-----YDSIESIVGS-PL 101
 Db 154 qnsqkvvgysfvegwgygrnftvdkipagqlthlygfipicgngindsikelegsfga 213
 QY 102 LFKSLGLEIYIGINEX-----FNDAMNLRKARPDIIIMLSLG 138
 Db 214 lqrsccgredfkisihdpfaalqkaqkyrtawddpykgnfgqimalkqhdpdlklpsig 273
 QY 139 GETYHPSSP-----DSALNAVEKIANLVDELFGDIDVDE---PNCSPFGCLNDKER 187
 Db 274 gwtlsdppffimgdkvkrdrtfvgsvkef--lgtwkffidgydidwefpgykganpnlgspqd 331
 QY 188 ADFVQYVYTKLREYMCDDKLISISQSSNGALSCIGFNDPKKICMDDEAPYNSKYFNKRPDV 247
 Db 332 getyvllmkelraml--dq1-----saetgryk----- 357
 QY 248 KKEILRAQMAASAGAIYLMNNLKMDIMVYOTFNT--NSTDSTVMKELYDSYAYYG 304
 Db 358 --eltsa---lsag-----kdkidkv--aynvagqsmhifilm---sydflyg 394

RESULT 9

ID AAM09402 standard; Protein; 561 AA.

AC AAM09402;

DT 19-FEB-1997 (first entry)

DE Serratia marcescens Chitinase A.

XX Chitinase; ChIA; chitin degradation; transgenic plant; tomato;

KW cold resistance; tolerance; frost damage; reducing sugar content;
 KW increase; ATCC 9901; ds.

XX Serratia marcescens QMB 1466.

OS Serratia marcescens QMB 1466.

XX Key Location/Qualifiers

FT Peptide 1..23 /label= signal_peptide

FT /note= "predicted cleavage site is between residues

FT Protein 24..561 /label= Chitinase_A

FT /note= "predicted mature sequence"

XX US554521-A.

XX 10-SEP-1996.

XX 26-MAR-1984; 84US-0593691.

XX 19-DEC-1994; 94US-0358901.

XX 26-MAR-1984; 84US-0593691.

PR 18-JUL-1986; 86US-0888033.
 PR 09-JUL-1990; 90US-0550253.
 PR 14-AUG-1992; 92US-0930970.

XX (DNAP) DNA PLANT TECHNOLOGY CORP.

XX Jones JDE, Suslow TV;

XX WPI: 1996-424655/42.

DR N-PSDB; AAT49479.

PT Recombinant plant with increased resistance to cold - and increased
 PT reducing sugar content, contains DNA encoding chitinase, partic. to
 PT protect tomatoes against frost damage.

XX Example 3; Fig 1A-C; 25pp; English.

CC The present sequence is the Chitinase A enzyme encoded by the 2.3 kb
 CC insert of plasmid pCHIT1251 which was isolated from genomic DNA of
 CC Serratia marcescens QMB 1466 (ATCC 9901). The chIA gene can
 CC be used for transforming plants, esp. tomatoes, to give increased
 CC resistance to frost damage and to produce sweeter fruit.

XX Sequence 561 AA;

Query Match 6.4%; Score 127.5; DB 17; Length 561;
 Best Local Similarity 23.2%; Pred. No. 0.0028;
 Matches 83; Conservative 44; Mismatches 114; Indels 117; Gaps 21;

QY 2 NFTV---KYSFLVYICLLC---CLSTYVSV---EGHRARPGESRKNP-REIITFK 48
 Db 99 ntkvknkgrygmqv--alcnadgctasdateivvadtdgshlpp---lkeplleknpkyk 153
 QY 49 ESGKGIIQGYPSWVSYNHNLK-DLNPNLNVHMSFAKMDLS-----YDSIESIVGS-PL 101
 Db 154 qnsqkvvgysfvegwgygrnftvdkipagqlthlygfipicgngindsikelegsfga 213
 QY 102 LFKSLGLEIYIGINEX-----FNDAMNLRKARPDIIIMLSLG 138
 Db 214 lqrsccgredfkisihdpfaalqkaqkyrtawddpykgnfgqimalkqhdpdlklpsig 273
 QY 139 GETYHPSSP-----DSALNAVEKIANLVDELFGDIDVDE---PNCSPFGCLNDKER 187
 Db 274 gwtlsdppffimgdkvkrdrtfvgsvkef--lgtwkffidgydidwefpgykganpnlgspqd 331
 QY 188 ADFVQYVYTKLREYMCDDKLISISQSSNGALSCIGFNDPKKICMDDEAPYNSKYFNKRPDV 247
 Db 332 getyvllmkelraml--dq1-----saetgryk----- 357
 QY 248 KKEILRAQMAASAGAIYLMNNLKMDIMVYOTFNT--NSTDSTVMKELYDSYAYYG 304
 Db 358 --eltsa---lsag-----kdkidkv--aynvagqsmhifilm---sydflyg 394

RESULT 10

ID AAM60179 standard; Protein; 561 AA.

AC AAM60179;

DT 03-SEP-1998 (first entry)

DE Serratia marcescens chitinase A sequence.

XX Chitinase A; pathogen; plant protection; Serratia marcescens; E. coli;

KW Pseudomonas; Erwinia; frost damage resistance; plant pathogen; fungus;
 KW nematode.

XX Serratia marcescens.

XX Key Location/Qualifiers

FT Peptide 1..23

```

FT      /note= "putative signal peptide"
FT      Cleaveage-site 23..24
FT      /note= "predicted cleavage site"
FT      Protein 24..561
FT      /note= "mature protein"
XX      US5776448-A.
XX      07-JUL-1998.
XX      01-AUG-1996; 96US-0693835.
XX      19-DEC-1994; 94US-0358901.
XX      26-MAR-1984; 84US-0593691.
XX      18-JUL-1986; 86US-0888033.
XX      09-JUL-1990; 90US-0550253.
XX      14-AUG-1992; 92US-0930970.
XX      01-AUG-1996; 96US-0693835.
XX      (DNAP ) DNA PLANT TECHNOLOGY CORP.
XX      Jones JDC, Suslow TV;
XX      WPI: 1998-397941/34.
XX      N-PSDB: AAV35601.
XX      Use of heterologous chitinase nucleic acid - for transforming
XX      bacteria or plants, for increasing plant resistance to plant
XX      pathogens, increase chilling resistance and increasing sweetness.
XX      Example 3; Fig 1A-C; 25pp; English.
XX      This represents a Serratia marcescens chitinase A. The invention
XX      provides a method for the production of a bacterial cell capable of
XX      producing chitinase which comprises transforming the bacterial cells
XX      with a nucleic acid encoding the chitinase, the nucleic acid being
XX      isolated from a heterologous source, and whereby the bacterial cell
XX      is capable of expressing the nucleic acid. The bacterial cell is selected
XX      from Pseudomonas sp., E. coli or Erwinia sp. The products can be used to
XX      enhance plant growth by biological control of plant pathogens such as
XX      fungi, nematodes, insects and disease agents. Plants transformed with
XX      the chitinase DNA can also have resistance to frost (freezing) damage
XX      or chilling damage, increased levels of reducing sugars or sweetness
XX      in fruits or plants and enhanced post-harvest storage life. The
XX      products can also be used for the production of chitinase for use as an
XX      antibiotic.
XX      Sequence 561 AA:
SQ
Query Match 6.4%; Score 127.5; DB 19; Length 561;
Best Local Similarity 23.2%; Pred. No. 0.0028;
Matches 83; Conservative 44; Mismatches 114; Indels 117; Gaps 21;
OY      2 NPTV-----KYSTLVLCILC-----CLSTYVSIT-----EGHRRPESKRNP-REITKTFK 48
DB      99 ntkvkggrygmqv--alcnadgctasdatelevadtgshlp---lkepllenknyk 153
OY      49 ESGKGIIGGYPSWVSYYHNLK-DLNPMLNYYHMSFAKMDLS-----YDSISIVGS-PL 101
DB      154 gnsqkvvsyfwewgvygrnftvdkipagntlhllygfipicgngindslleagstfqa 213
OY      102 LFKSLIGLEYIGLNEY-----FNDAMNLRARPDIIMLSIG 138
DB      214 lgrscgqredfkshdpfaalqkqkqvtawddpykgnfgqlmalakqahpdlkflpsig 273
OY      139 GETYRPSF-----DSALNAVEKIANLVEDELFGDIDVDF--FNGSDGLNDKEX 187
DB      274 gwtlsdpifmgdkvkrrfygsvkef--lqtwkftfdgvdidwefpggkyganpnlgspqd 331
OY      188 ADFEVOYTKLREYWCDDKLISISQSSNGALSCIGFNDPKRCICMDEAPKSYFNKPDV 247
DB      332 getyvlmkelraml--dqI-----saetgrky----- 357

```

```

OY      248 KELLRAQMASAGAIYIMNLIKMDIDVEVQTFENYT-NSDSTVMEKELYDVAAYG 304
DB      358 --eltsa---lsag-----kdkldkv---aynvagumdhiflm-----sydfyg 394

RESULT 11
AAV52523
ID      AAV52523 standard; Protein; 555 AA.
XX      AAV52523;
XX      22-FEB-2000 (first entry)
XX      House dust mite (D. farinae) mite allergen protein (map) Pderf98-555.
XX      Mite allergen protein; map; high molecular weight; HmW-map; allergy;
XX      house dust mite; IgE; immunoglobulin E; allergen; mapA; mapB;
XX      hypersensitivity reaction; therapy; treatment; diagnosis; human; feline;
XX      canine; veterinary; antibody; vaccine; immunisation.
XX      Dermatophagoides farinae.
XX      OS
XX      Key Location/Qualifiers
XX      Peptide 1..19
XX      /note= "Signal peptide"
XX      Protein 20..555
XX      /note= "Mature Pderf98-555"
XX      W09954349-A2.
XX      28-OCT-1999.
XX      16-APR-1999; 99WO-US08524.
XX      17-APR-1998; 98US-0062013.
XX      13-MAY-1998; 98US-0085295.
XX      02-SEP-1998; 98US-0098909.
XX      (HESK-) HESKA CORP.
XX      McCall CA, Hunter SW, Weber ER;
XX      WPI: 2000-052700/04.
XX      N-PSDB: AAZ38575, AAZ38576, AAZ38577, AAZ38578.
XX      Novel high molecular weight Dermatophagoides nucleic acid polypeptides
XX      used to modify an animals' hypersensitivity to mite allergens
XX      Claim 3; Page 111-113; 154pp; English.
XX      This sequence represents Dermatophagoides farinae mite allergen protein
XX      (map) Pderf98-555. Pderf98-555 has a molecular weight of 98 kD,
XX      comprising 555 amino acids, and is a component of the Dermatophagoides
XX      farinae high molecular weight mite allergen protein (HmW-map)
XX      composition. The HmW-map composition was isolated from a D. farinae
XX      homogenate by gel filtration, with each fraction being analysed for
XX      the presence of proteins that bound to IgE present in mite-allergic
XX      dog antisera. Mite allergenic proteins and peptides, and nucleic acids
XX      encoding them, may be used in therapeutic compositions to modify an
XX      animal's hypersensitivity reaction to mite allergens. Animals that
XX      may be treated include mammals and birds, especially felines,
XX      canines, equines, humans, other pets, and work or domestic
XX      animals. The proteins or fragments may also be used to diagnose
XX      allergies via a skin test. The proteins and peptides can also
XX      be used to raise antibodies, which have a variety of potential
XX      uses. For example, they can be used as vaccines to passively immunise
XX      animals against dust mite hypersensitivity, as positive controls in
XX      test kits and as tools to recover desired dust mite allergens from a
XX      mixture of proteins.
XX      Sequence 555 AA:
SQ

```

Query Match 6.4%; Score 126; DB 21; Length 555;
 Best Local Similarity 21.2%; Pred. No. 0.0039;
 Matches 95; Conservative 57; Mismatches 160; Indels 136; Gaps 25;

```

OY 5 VKISFLVICLLCLLSIVSYIEGHRARPGESRKNPREITTFKESGKGIIGYPSNVS 64
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   1 mktiyalalsimacglnmaslkrth-----ndysknpmriv-----cygwtsv 44
DB
OY 65 YN-----HNLEDLNPNLVNVMH--SFAKMDLSYDSIESIVGSPLLFKSLIGLEYIGLN 118
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   45 ykhvdyttiedip-fccthlmygfakideyktyiq--vfipygdannswekrgy-erf 100
DB
OY 119 NDAMNLRKARPDIIIMLSLG-----ETYPSSFDSALNA-----VEKIANLVDELGFD 167
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   101 n--nrlknpeltmtislsgwygsekys-----dmanptryqgfdlqeykfd 153
DB
OY 168 GIDVDEPNNSFDG-----LND-----KEKAD--FFVQY 194
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   154 gllddeyppsrjgnpkidqnylalvrelkdafehylltaavspgkdkidraydike 213
DB
OY 195 VTKLREVMCDKLISISQSGNALSCIGFNDP--KKICMDDE-----APYNSKYF-NKP 245
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   214 lnlfdm-----nmtydyngwenfygnaplykrpdetelhtyfnvnytmbylmg 269
DB
OY 246 DVKELIRAAQMASAGAIYLMNL-----KDMIDVFOV-----TFNYTSTDSVWKE 295
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   270 atrdklvmgvpfygrawledrsklikgdpakgmsppgisgeegvlsielcqlfgk 329
OY 296 LVDSY-AVYGKKYDYVIMGFILMFSTPFNPNDKMLVKSIGDFVKTENKL-----NKRAD 350
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   330 whqydeyynapygy-----ndkiwv-gyddlaaslscklaflkelgvs 371
DB
OY 351 GFGLWSTLSD-----NAAHN 365
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   372 gymvwalenddfkghgkpnllnkvn 399
DB

```

RESULT 12

AAR63441
 ID AAR63441 standard; Protein; 424 AA.

AC AAR63441;

DT 06-JUL-1995 (first entry)

DE Trichoderma harzianum P1 endochitinase.

KW Trichoderma harzianum P1: endochitinase: inhibition;

KW chitin containing fungi; herbivorous insects.

OS Trichoderma harzianum.

PN WO9424288-A.

PD 27-OCT-1994.

PF 10-FEB-1994; 94WO-US01198.

PR 14-APR-1993; 93US-0045269.

PA (CORR) CORNELL RES FOUND INC.

PI Harman GE, Hayes CK, Lorito M, Tronsmo A;

DR WPI: 1994-341867/42.

DR N-PSDB; AAQ78144.

PT Trichoderma harzianum P1 endo:chitinase and chitinase genes -
 useful in biological control of chitin-contg. fungi and insects
 (Eng).

PS Example 8; Page 45; 62pp: English.

XX AAQ78144 encodes AAR63441 the Trichoderma harzianum P1 endochitinase,
 CC which can be used to inhibit chitin containing fungi and chitin
 CC containing herbivorous insects, especially from the genera below
 CC Fusarium, Gliocladium, Rhizoctonia, Trichoderma, Uncinula, Ustilage,
 CC Erysiphe, Botrytis, Sclerotium, Sclerotium and Alternaria.
 SO Sequence 424 AA;

Query Match 6.3%; Score 124.5; DB 15; Length 424;
 Best Local Similarity 21.0%; Pred. No. 0.0036;
 Matches 65; Conservative 51; Mismatches 93; Indels 101; Gaps 14;

```

OY 58 YPSPVSNHMLKDLN-PNLNVNHSFAKMDL-SYDSIESIVGSPLLFKSLIGLEYIGLN 115
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   44 yftmgylgrnlfqpnlvassdltlvysfmlleaygtvs-----gdayedq 91
DB
OY 116 EYFND-----AMNLRKARPDIIIMLSLGCTYPSSFDSAL-----N 152
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   92 khyddswndvgnnaygcvkqlfkikangnlkwmislsgwtv--stnfpaastdanrkn 150
DB
OY 153 AVEKIANLVDELGFDGIDVDEPNNSFDGLNDEKADFEVQYVTKLREVMCDKLISISQ 212
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   151 fakatitmkdwgfygldvaw-----eypad-----tq 179
DB
OY 213 SSNGALSCIGFNDPKKICMDDEAPYNSKYFNKPDVKELIRAAQMASAGAIYLMNLKD 272
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   180 atnmvlll-----keirsglda-yaagy--apgyhflslsaapagheysflmsdlgq 230
DB
OY 273 MIDVFOVTFNYTSTDSVWKELYDSAYYGGKKYDYVIMGFILMFSTPFNPNDK--M 330
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   231 vldvnmayyags-----wssys-----ghdanlfanpsnpsyn 269
DB
OY 331 LVKSIGDFVK 340
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   270 tdgaikgyik 279
DB

```

RESULT 13

AAY52535
 ID AAY52535 standard; Protein; 490 AA.

AC AAY52535;

DT 22-FEB-2000 (first entry)

DE D. pteronyssius 98 kD mite allergen protein (map) pDerp98-490.

KW Mite allergen protein; map; high molecular weight; HMW-map; allergy;

KW house dust mite; IGE; immunoglobulin E; allergen; mapB;

KW hypersensitivity reaction; therapy; treatment; diagnosis; human; feline;

KW canine; veterinary; antibody; vaccine; immunisation.

OS Dermatophagoides pteronyssius.

PN Key Location/Qualifiers

FT Modified-site 115..117 /note="Asn is N-glycosylated"

FT Modified-site 240..242 /note="Asn is N-glycosylated"

PN WO9954349-A2.

PD 28-OCT-1999.

PF 16-APR-1999; 99WO-US08524.

PR 17-APR-1998; 98US-0062013.

PR 13-MAY-1998; 98US-0085295.

PR 02-SEP-1998; 98US-0098909.

PA (HESK-) HESKA CORP.

```

XX  McCall CA, Hunter SW, Weber ER;
PI
XX
XX  WPI: 2000-052700/04.
DR  N-PSDB: AAZ38589, AAZ38590.
XX
XX  Novel high molecular weight Dermatophagoides nucleic acid polypeptides
PT  used to modify an animals' hypersensitivity to mite allergens
XX
XX  Claim 3; Page 147-149; 154pp; English.
XX
XX  This sequence represents Dermatophagoides pteronyssinus mite allergen
CC  protein (map) pDerp98-490, the mature form of pDerp98-509. pDerp98-490
CC  has a molecular weight of 98 kD, comprising 490 amino acids, and
CC  has a high degree of homology with the D. farinae mature 98 kD
CC  allergen, mapB (AAV52525). Nucleic acid molecules encoding
CC  pDerp98-490 were isolated from a D. pteronyssinus cDNA library by
CC  hybridisation with a probe encoding the D. farinae high molecular
CC  weight map (HMW-map) composition. Mite allergenic proteins and
CC  peptides, and nucleic acids encoding them, may be used in therapeutic
CC  compositions to modify an animal's hypersensitivity reaction to mite
CC  allergens. Animals that may be treated include mammals and birds,
CC  especially felines, canines, equines, humans, other pets, and work or
CC  domestic animals. The proteins or fragments may also be used to
CC  diagnose allergies via a skin test. The proteins and peptides can also
CC  be used to raise antibodies, which have a variety of potential
CC  uses. For example, they can be used as vaccines to passively immunise
CC  animals against dust mite hypersensitivity, as positive controls in
CC  test kits and as tools to recover desired dust mite allergens from a
CC  mixture of proteins.
XX
XX  Sequence 490 AA:
SQ

```

Query Match
Best Local Similarity 22.8%; Score 122.5; DB 21; Length 490;
Matches 78; Conservative 45; Mismatches 110; Indels 109; Gaps 19;

```

OY  38 KNPREIITFKESGKGIIGYPPSVSYN---HNKLDLPNLNVHM--SFAKMDLSTD 91
DB  11 knpmfiv-----cygltwsvyhkvdpyctledidp-fkctthmygfakideky 57
OY  92 STESIVGSPLEKSLIGLEYGLNEFYNDAMNLRKARPDITMLSLGSG---EYVHPSS 146
DB  58 tiq--vifpfdqdmnqyehky-erfn---nlrlkpelitmtislgwyegsekyss--- 108
OY  147 FDSALNA-----VEKINLVDELGFDGIDVDYEPNGSFDGLNDEKADDFVQYVTKLRE 200
DB  109 -dmanpnyrqfvgsvldifqeykfkgldidweygsrlg-nplidkqnyltlvrelke 166
OY  201 YWCDDKLISISOSNGALSCIGFENDPKKICMDEAPYNSKYFNKPDVKKELLRAAOMASA 260
DB  167 -----alepfgy-----lltaa--vsp 181
OY  261 G----GATILMNMLKMDMWFVQFENTNSTDSV-----MKELYDXYAYYCKRY 307
DB  182 9kdkldavejelkeInqlIdammvmcydyhgwenvfghnaplykrpdecelhcyfnyv 241
OY  308 --DYVIMGFT-----LMFPSTFPNPNDKMLVKSIGDFVK 340
DB  242 tmhyllngatrdkiymgvpfygrawsledrskvr-ldgdpak 282

```

RESULT 14
AAV51402
ID AAV51402 standard; Protein: 424 AA.
XX
XX AAV51402;
AC
XX 04-MAY-2000 (first entry)
DT
XX
XX T. harzianum strain PI endochitinase protein.
DE
XX

```

KW  Endochitinase; pesticide; chitin degradation; fungi; insect.
XX
XX  Trichoderma harzianum.
OS
XX
XX  US6020540-A.
PN
XX
XX  01-FEB-2000.
PD
XX
XX  21-DEC-1994; 94US-0371680.
PF
XX
XX  17-JUN-1991; 91US-0716134.
PR  27-JUL-1992; 92US-0919784.
PR  15-DEC-1992; 92US-0990609.
PR  14-APR-1993; 93US-0045269.
PR  21-APR-1993; 93US-0049390.
PR  21-JAN-1994; 94US-0184115.
XX
XX  (CORR ) CORNELL RES FOUND INC.
XX
XX  Harman GE, Tronsmo A, Hayes CK, Klemisdahl S, Iorito M;
PI
XX
XX  WPI: 2000-146920/13.
DR  N-PSDB: AAZ88577.
XX
XX  DNA encoding endochitlinases, useful as environmentally friendly
PT  pesticides -
XX
XX  Claim 28; Column 25-28; 30pp; English.
XX
XX  This invention describes novel endochitinase peptides isolated from
CC  Trichoderma harzianum strain PI which have pesticidal activity. The
CC  endochitinase degrades the chitin present in fungi and insects and
CC  therefore the products of the invention are useful as pesticides for
CC  biological control of chitin-containing fungi and insects. The use of
CC  endochitlinases avoids environmental pollution and ecological disruption.
CC  Assays for the inhibition of the plant pathogen Botrytis cinerea were
CC  carried out in microtiter plates and observed after 24 hours with an
CC  inverted microscope. Ampicillin was used to prevent bacterial growth
CC  during the assay. Hyphal elongation was inhibited by 5.5, 24 and 548
CC  using 1, 5 and 10 micro g/ml of endochitinase, respectively and spore
CC  germination was inhibited by 5.5, 25 and 518 using 1, 5 and 10 micro
CC  g/ml, respectively. This sequence represents the T. harzianum
CC  endochitinase protein used in the method of the invention.
XX
XX  Sequence 424 AA:
SQ

```

Query Match
Best Local Similarity 20.7%; Score 120.5; DB 21; Length 424;
Matches 64; Conservative 50; Mismatches 96; Indels 99; Gaps 14;

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OY  58 YPSWVSYNHNKLDLN-PNINLVHMSFAKMDLSYDSIESIVGSPLEKSLIGLEYGLNE 116
DB  44 yftngwiygrnqpnlvdsdlthvysfmmfagd--lvvs-----gdayedqyk 92
OY  117 YFND-----AMNLRKARPDITMLSLGSETYVHPSSFDAL-----NA 153
DB  44 yftngwiygrnqpnlvdsdlthvysfmmfagd--lvvs-----gdayedqyk 92
OY  93 hyddswndvgnaygcvkqkfkikkanrnllkvmislgwtv-stnfiaaastdanrkf 151
DB  154 VEKINLVDELGFDGIDVDYEPNGSFDGLNDEKADDFVQYVTKLREYWCDDKLISISOS 213
DB  152 aktaalfmkdwfgdgdvaw-----eypadt-----tga 180
OY  214 SNGALSCIGFENDPKKICMDEAPYNSKYFNKPDVKKELLRAAOMASAGATILMNMLKMD 273
DB  181 tmvnlill-----kelrsglda-yaagy--apgyhllislaapagehysflhmsdlyqv 231
OY  274 IDMFVQFENTNSTDSVYMKELYDSYAYYGGKRYDVIIMGFTLMFPSTFPNPNDK--ML 331
DB  232 ldyvnlmaydyags-----wssys-----gndanlfanpsnpnspsynt 270
OY  332 VKSIGDFVK 340

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 8, 2002, 08:57:07 ; Search time 12.57 Seconds

(without alignments)
676,710 Million cell updates/sec

Title: US-09-579-383-3

Perfect score: 1982
Sequence: 1 MNFTYKYSFLVLCILCLLS.....SDNAHNEQLATIEYFESLH 378

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Issued Patents.AA.*

1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep.*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep.*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep.*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep.*
5: /cgn2_6/ptodata/2/1aa/PTCUS.COMB.pep.*
6: /cgn2_6/ptodata/2/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	135.5	6.8	298	3	US-09-025-691-1
2	127.5	6.4	561	1	US-08-358-901-2
3	127.5	6.4	561	1	US-08-566-347-2
4	127.5	6.4	561	1	US-08-693-835-2
5	124.5	6.3	424	5	PCT-US94-01198-2
6	120.5	6.1	424	1	US-08-045-269C-2
7	120.5	6.1	424	3	US-08-371-680-2
8	117.5	5.9	866	1	US-08-386-727-8
9	117.5	5.9	866	2	US-08-600-452A-8
10	111	5.6	461	2	US-08-392-625-24
11	111	5.6	461	2	US-08-466-961A-24
12	111	5.6	461	2	US-08-645-193B-26
13	110.5	5.6	376	3	US-09-025-691-3
14	108.5	5.5	1453	1	US-08-308-872B-6
15	107	5.4	554	2	US-08-524-051-2
16	107	5.4	554	2	US-09-052-778-16
17	102	5.1	327	3	US-08-926-724-3
18	102	5.1	1046	1	US-08-904-032-3
19	101.5	5.1	1046	1	US-08-386-727-2
20	101.5	5.1	1046	2	US-08-600-452A-2
21	100.5	5.1	423	1	US-07-939-501A-10
22	100.5	5.1	423	1	US-07-939-501A-12
23	100	5.0	440	3	US-09-052-778-13
24	99.5	5.0	389	1	US-07-939-501A-1
25	99.5	5.0	389	4	US-08-448-398-7
26	99.5	5.0	1452	2	US-08-331-625A-2
27	99.5	5.0	1452	5	PCT-US93-04384-18

28	99.5	5.0	1452	5	PCT-US93-04692-2	Sequence 2, Appli
29	98	4.9	128	3	US-08-331-625A-51	Sequence 51, Appl
30	98	4.9	250	3	US-08-331-625A-57	Sequence 57, Appl
31	98	4.9	327	2	US-08-926-724-1	Sequence 1, Appli
32	98	4.9	362	3	US-08-331-625A-53	Sequence 53, Appl
33	98	4.9	1443	1	US-08-308-872B-2	Sequence 2, Appli
34	98	4.9	1454	4	US-08-392-459-32	Sequence 32, Appl
35	98	4.9	1454	4	PCT-US91-08525-32	Sequence 32, Appl
36	98	4.9	1454	5	PCT-US93-04384-12	Sequence 12, Appl
37	98	4.9	1454	5	PCT-US93-04384-43	Sequence 43, Appl
38	98	4.9	1454	5	PCT-US93-04384-46	Sequence 46, Appl
39	98	4.9	1454	5	PCT-US93-04384-48	Sequence 48, Appl
40	97.5	4.9	720	2	US-08-840-236-1	Sequence 1, Appli
41	97.5	4.9	720	2	US-08-505-448A-1	Sequence 1, Appli
42	97.5	4.9	1346	1	US-08-471-033-23	Sequence 23, Appl
43	97.5	4.9	1346	2	US-08-471-044-23	Sequence 23, Appl
44	97.5	4.9	1346	2	US-08-463-483A-23	Sequence 23, Appl
45	97.5	4.9	1346	2	US-08-471-046A-23	Sequence 23, Appl

ALIGNMENTS

```
RESULT 1
US-09-025-691-1
; Sequence 1, Application US/09025691
; Patent No. 6069299
; GENERAL INFORMATION:
; APPLICANT: Broadway, Roxanne M.
; TITLE OF INVENTION: FUNGUS AND INSECT CONTROL WITH
; TITLE OF INVENTION: CHITINOLYTIC ENZYMES
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESS: Nixon, Hargrave, Devans & Doyle LLP
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025, 691
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldman, Michael L.
; REGISTRATION NUMBER: 30,727
; REFERENCE/DOCKET NUMBER: 19603/20120
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 263-1304
; TELEFAX: (716) 263-1600
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 298 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-025-691-1

Query Match 6.8%; Score 135.5; DB 3; Length 298;
Best Local Similarity 21.7%; Pred. No. 2.5e-05;
Matches 55; Conservative 50; Mismatches 76; Indels 73; Gaps 12;

Oy 55 IGGYPPSVNHN-----NKDNLNINLVHMFKMDLSYDSISYIGSPLLFSLGL 109
Db 10 VTGT---WQNNKATVOTLADVPDAVDIIAVSFADATAMAGET-----TFTL 54
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[illegible]

```

RESULT 2
US-08-358-901-2
Sequence 2, Application US/08358901
Patent No. 5554521
GENERAL INFORMATION:
APPLICANT: Suslow, Trevor V.
APPLICANT: Jones, Jonathan D.G.
TITLE OF INVENTION: No. 5554521el Chitinase-Producing Plants
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/358,901
FILING DATE: 19-DEC-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/550,253
FILING DATE: 09-JUL-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/888,033
FILING DATE: 18-JUL-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/593,691
FILING DATE: 26-MAR-1984
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 12176-5-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 561 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-358-901-2

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Query Match	6.48;	Score 127.5;	DB 1;	Length 561;
Best Local Similarity	23.2%;	Pred. No. 0.0004;		
Matches	83;	Conservative 44;	Mismatches 114;	Indels 117;
			Gaps	21.

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Db      99  NFKVNGGRYQMOV--ALCNADGCTASDATEIVADYIDGSHLP-----LKEBLLKNNPK 153B
OY      49  ESGKTIIOGYIPSWSYHNHK-DLNPPLNVNHSFAKMDLS-----YDSTESYGS-PL 101B
Db      154  QNSGRVSYSEYVEMGVYGRNPTVDKIPANLTHLLYGFIPLCGGNGJINDSLKEIEGFSFOA 213B
OY      102  LFKSLIGLEYTGLNRY-----FMDANNLRKRPDITIMLSIG 138B
Db      214  LQRSQGGEDERKISHDFPALQQAQGYATMNDPYPKNGNGQMLMALQAPDLKILPISIG 273B
OY      139  GETYHPSSF-----DSALNAVEKIANLYDELGFQIDVYE--PNSGFDGLNDREK 187B
Db      274  GWTLSDPFPFFMGDKRKDRPFGSVKEF--LQTKWFFEGVDIDMEFPGCKANPILGSPQD 331B
OY      188  ADFEPQYVTKRLREIMCDKLLISIQSSNGALSCIGFNDPPKICMDDEAPINSKYFNKPDV 247B
Db      332  GETYVLLMKELRAML--DOL-----SAETGRRY-----357B
OY      248  KKELLRAQAQMSAGCAIYIMNLKMDIMDVFEQTFNYT--NSTDSTVYKELDYSAAYYG 304B
Db      358  --ELTSA--ISAG-----KDKIDKY--AYNNAQMSMHITFLM-----SYDFYG 394B

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RESULT 3
 US-08-566-347-2
 Sequence 2, Application US/08566347
 Patent No. 5633450
 GENERAL INFORMATION:
 APPLICANT: Suslow, Trevor V.
 APPLICANT: Jones, Jonathan D.G.
 TITLE OF INVENTION: No. 5633450el Chitinase-Producing Plants
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend Kourie and Crew
 STREET: One Market Plaza, Stewart Tower, Suite 2000
 City: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94105
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/566,347
 FILING DATE: 01-DEC-1995
 CLASSIFICATION: 800
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/358,901
 FILING DATE: 19-DEC-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/550,253
 FILING DATE: 09-JUL-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 06/888,033
 FILING DATE: 18-JUL-1986
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 06/593,691
 FILING DATE: 26-MAR-1984
 ATTORNEY/AGENT INFORMATION:
 NAME: Smith, William M.
 REGISTRATION NUMBER: 30,223
 REFERENCE/DOCKET NUMBER: 12176-5-3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-326-2400
 TELEFAX: 415-326-2422
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 561 amino acids
 TYPE: amino acid
 TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-566-347-2

Query Match 6.4%; Score 127.5; DB 1; Length 561;
Best Local Similarity 23.2%; Pred. No. 0.0004;
Matches 83; Conservative 44; Mismatches 114; Indels 117; Gaps 21;

QY 2 NFTV---KSFVVICLLC---CLSTYVSYI---EGHRRAPGESRKNP-REIKTFK 48
DB 99 NFKVKKGRYQMOV--ALCNADGCTASDATEIYVADTGSHP--LKEPLLEKKNPKYK 153
QY 49 ESKGIIIGYVPSWVSYNHNK-LDLPNLNVYHMSFAKMDLS---YDSTESIVGS-PL 101
DB 154 QNSGKVVSIFYEMGVGRNFTVDKIPAOHLTHLYGFIPICGGINDSLKEIGSFQA 213
QY 102 LFKSLIGLEYIGLNEY-----FNDAMNLKRAPDIIIMLSIG 138
DB 214 LQSCQGRDEPKISIHDPFALQKQKGTAMDPPYKGNFQGLMALKQAHPLKILPSIG 273
QY 139 GETYHPSSF-----DSALNAVERKIANLYDELGFDGIDVYE---PNSGFDGLNDEK 187
DB 274 GWTLSDFPFMGDKVKRRRFVGSVKEF--LQTKRFDDVIDMERPGKGAPNNGSPQD 331
QY 188 ADFEYQVYTKLREYWCDDKLISISQSSNGALSCIGFNDPKKICMDEAPYNSKYFNKPDV 247
DB 332 GETYVLLKKELRAML--DQL-----SAETGRKY----- 357
QY 248 KKEILRAAOMASAGAIYLMNNLKMDIDMVFYQFENYT--NSTDSTVMKELDSYAYYG 304
DB 358 --ELTSA---ISAG-----KDKIDKV---AYNVAQNSMDHIFLM---SYDFYG 394

RESULT 4

US-08-693-835-2
Sequence 2, Application US/08693835
Patent No. 5776448
GENERAL INFORMATION:
APPLICANT: Suslow, Trevor V.
APPLICANT: Jones, Jonathan D.G.
TITLE OF INVENTION: No. 5776448el Chitinase-Producing Plants
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/693,835
FILING DATE: 01-AUG-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/358,901
FILING DATE: 19-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/550,253
FILING DATE: 09-JUL-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/888,033
FILING DATE: 18-JUL-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/593,691
FILING DATE: 26-MAR-1984
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223

REFERENCE/DOCKET NUMBER: 12176-5-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 561 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-693-835-2

Query Match 6.4%; Score 127.5; DB 1; Length 561;
Best Local Similarity 23.2%; Pred. No. 0.0004;
Matches 83; Conservative 44; Mismatches 114; Indels 117; Gaps 21;

QY 2 NFTV---KSFVVICLLC---CLSTYVSYI---EGHRRAPGESRKNP-REIKTFK 48
DB 99 NFKVKKGRYQMOV--ALCNADGCTASDATEIYVADTGSHP--LKEPLLEKKNPKYK 153
QY 49 ESKGIIIGYVPSWVSYNHNK-LDLPNLNVYHMSFAKMDLS---YDSTESIVGS-PL 101
DB 154 QNSGKVVSIFYEMGVGRNFTVDKIPAOHLTHLYGFIPICGGINDSLKEIGSFQA 213
QY 102 LFKSLIGLEYIGLNEY-----FNDAMNLKRAPDIIIMLSIG 138
DB 214 LQSCQGRDEPKISIHDPFALQKQKGTAMDPPYKGNFQGLMALKQAHPLKILPSIG 273
QY 139 GETYHPSSF-----DSALNAVERKIANLYDELGFDGIDVYE---PNSGFDGLNDEK 187
DB 274 GWTLSDFPFMGDKVKRRRFVGSVKEF--LQTKRFDDVIDMERPGKGAPNNGSPQD 331
QY 188 ADFEYQVYTKLREYWCDDKLISISQSSNGALSCIGFNDPKKICMDEAPYNSKYFNKPDV 247
DB 332 GETYVLLKKELRAML--DQL-----SAETGRKY----- 357
QY 248 KKEILRAAOMASAGAIYLMNNLKMDIDMVFYQFENYT--NSTDSTVMKELDSYAYYG 304
DB 358 --ELTSA---ISAG-----KDKIDKV---AYNVAQNSMDHIFLM---SYDFYG 394

RESULT 5

PCT-0594-01198-2
Sequence 2, Application PC/TUS9401198
GENERAL INFORMATION:
APPLICANT: Harman, Gary E.
APPLICANT: Tronsmo, Arne
APPLICANT: Hayes, Christopher K.
TITLE OF INVENTION: Gene Encoding for Endochitinase
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spector, Eric S.
STREET: P.O. Box 2266 Bads Station
CITY: Arlington
STATE: Virginia
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/01198
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/045,269
FILING DATE: 14-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Spector, Eric S.

REGISTRATION NUMBER: 22495
REFERENCE/DOCKET NUMBER: CRF-D1060C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-415-1500
TELEFAX: 703-415-1508
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 424 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US94-01198-2

Query Match 6.3%; Score 124.5; DB 5; Length 424;
Best Local Similarity 21.0%; Pred. No. 0.00052;
Matches 65; Conservative 51; Mismatches 93; Indels 101; Gaps 14;

QY 58 YPSWVSYNHNLKDLN-PNLNVHMSFAKMDL-STDSIESIVGSPFLKSLGLEIYGLN 115
DB 44 YFTNWGIYGRNFPQNLVASDITHVIYSFMNLEAYGVVVS-----GDAYADYQ 91
QY 116 EYFND-----AMNLRKAPDIIMLSIGGETYHSPFSAL-----N 152
DB 92 KHYDDSDWNVGNNAVCYKQLEFKLRANGLKWLSTIGWTW-STNPPSAASTDANKRN 150
QY 153 AVEKIANLVDELGFIDVDEPEPNSGFDGLNDEKADFFVQVTKLREYMCDDKLISIQ 212
DB 151 FAKTATTFMKDWMGFDGIDVDM-----EYPADD-----TQ 179
QY 213 SSNGALSCIGFNDPKKICMDEAPYNSKYFNKPDVKKELLRAQMASAGAIYLMNNLKD 272
DB 180 ATNMVLL-----KEIRSQLDA-YAAQY-APGYHFLSLTAAPAGPHEYSFLHMSDGLQ 230
QY 273 MIDMVFQTFNTNSTSTYMKELDYSAAYGKKYDYIINGFTLMFSTPFNPNDK-M 330
DB 231 VLDYVNLMAADYAGS-----WSSYS-----GHDAFLFANPSNPNSSPYN 269
QY 331 LKVSIGDFVK 340
DB 270 TDQAIKDYIK 279

RESULT 6
US-08-045-269C-2
Sequence 2, Application US/08045269C
Patent No. 5378821
GENERAL INFORMATION:
APPLICANT: Hartman, Gary E.
APPLICANT: Tronsmo, Arne
APPLICANT: Hayes, Christopher K.
APPLICANT: Loritto, Matteo
TITLE OF INVENTION: Gene Encoding for Endochitinase
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones, Tullar & Cooper, P.C.
STREET: P.O. Box 2266 Eads Station
CITY: Arlington
STATE: Virginia
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/045,269C
FILING DATE: 14-APR-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/919,784
FILING DATE: 27-JUL-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/716,134
FILING DATE: 17-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Spector, Eric S.
REGISTRATION NUMBER: 22495
REFERENCE/DOCKET NUMBER: CRF-D1060C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-415-1500
TELEFAX: 703-415-1508
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 424 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-045-269C-2

Query Match 6.1%; Score 120.5; DB 1; Length 424;
Best Local Similarity 20.7%; Pred. No. 0.0013;
Matches 64; Conservative 50; Mismatches 96; Indels 99; Gaps 14;

QY 58 YPSWVSYNHNLKDLN-PNLNVHMSFAKMDLSTDSIESIVGSPFLKSLGLEIYGLN 116
DB 44 YFTNWGIYGRNFPQNLVASDITHVIYSFMNFOADG--TVVS-----GDAYADYQ 92
QY 117 YFND-----AMNLRKAPDIIMLSIGGETYHSPFSAL-----NA 153
DB 93 HYDDSDWNVGNNAVCYKQLEFKLRANGLKWLSTIGWTW-STNPPSAASTDANKRN 151
QY 154 VEKIANLVDELGFIDVDEPEPNSGFDGLNDEKADFFVQVTKLREYMCDDKLISIQS 213
DB 152 AKTATTFMKDWMGFDGIDVDM-----EYPADD-----TQA 180
QY 214 SSNGALSCIGFNDPKKICMDEAPYNSKYFNKPDVKKELLRAQMASAGAIYLMNNLKD 273
DB 181 TNMVLL-----KEIRSQLDA-YAAQY-APGYHFLSLTAAPAGPHEYSFLHMSDGLQ 231
QY 274 IDMFVQTFNTNSTSTYMKELDYSAAYGKKYDYIINGFTLMFSTPFNPNDK-ML 331
DB 232 LDYVNLMAADYAGS-----WSSYS-----GHDAFLFANPSNPNSSPYNT 270
QY 332 VKSIGDFVK 340
DB 271 DQAIKDYIK 279

RESULT 7
US-08-371-680-2
Sequence 2, Application US/08371680
Patent No. 6020540
GENERAL INFORMATION:
APPLICANT: Hartman, Gary E.
APPLICANT: Tronsmo, Arne
APPLICANT: Hayes, Christopher K.
APPLICANT: Loritto, Matteo
APPLICANT: Di Pietro, Antonio
TITLE OF INVENTION: Gene Encoding Endochitinase
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones, Tullar & Cooper, P.C.
STREET: P.O. Box 2266 Eads Station
CITY: Arlington
STATE: Virginia
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

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: APPLICATION NUMBER: US/08/371,680
: FILING DATE:
: CLASSIFICATION: 536
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/045,269
: FILING DATE: 14-APR-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/919,784
: FILING DATE: 27-JUL-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/716,134
: FILING DATE: 17-JUN-1991
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/184,115
: FILING DATE: 21-JAN-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/049,390
: FILING DATE: 21-APR-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/990,609
: FILING DATE: 15-DEC-1992
: ATTORNEY/AGENT INFORMATION:
: NAME: Spector, Eric S.
: REGISTRATION NUMBER: 22495
: REFERENCE/DOCKET NUMBER: CRF-D1424A
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 703-415-1500
: TELEFAX: 703-415-1508
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 424 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-371-680-2

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Query Match      6.1%; Score 120.5; DB 3; Length 424;
Best Local Similarity 20.7%; Pred. No. 0.0013;
Matches 64; Conservative 50; Mismatches 96; Indels 99; Gaps 14;

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QY 58 YPSVSVNHLKDLN-PNLNVVHMSFAKMDLSYDSISYGPLRFLSLGLEIYGLNE 116
D 44 YFTMGITGRNFPONLVASDITHYISFMNFQADG--TVVS-----GDATADYOK 92
QY 117 YFND-----AMNLRKARPDIIIMLSLGETYHPSPFSAL-----NA 153
D 93 HYDDSDMVDGNNAVGCWKJFKLKRANRLKMLSIGWTW-STNFPASASTDANRRNF 151
QY 154 VEKIANLYDELGFPGIDVDYEPNGSFDGLNDEKADFFVQYVTKLREYMCDDKLISISQS 213
D 152 AKTATTEPKMDGFPDIDVM-----EYPADD-----TQA 180
QY 214 SNGALSCGFGDPKICMDDEAPYNSKYENKPDYKELLRAAQMASAGALIYIMNLM 273
D 181 TMMVLL-----KEINSQIDA-YAAQY--APGYHFLSLIAPAGPEHYSELHMSDLCQV 231
QY 274 IDAVFVQTFNTNSTDSTVMKELDYSAVYGRKDYVILMGFTLFPSTPPNPNDK--ML 331
D 232 LDYVNLMAVDYAGS-----WSSYS-----CHDANLFPANPSNPSPNT 270
QY 332 VKSIGDFVK 340
D 271 DOAIRDYIK 279

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RESULT 8
US-08-386-727-8
: Sequence 8, Application US/08386727
: Patent No. 5792647
: GENERAL INFORMATION:
: APPLICANT: ROSEMAN, SAUL
: APPLICANT: BASSLER, BONNIE

```

```

: APPLICANT: KEYHANI, NEMAT O.
: APPLICANT: CHITLARD, EDITH
: APPLICANT: ROME, CHRIS
: APPLICANT: YU, CHARLES
: TITLE OF INVENTION: BACTERIAL CATABOLISM OF CHITIN
: NUMBER OF SEQUENCES: 8
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
: STREET: 1100 NEW YORK AVENUE, N.W.
: CITY: WASHINGTON
: STATE: D.C.
: COUNTRY: USA
: ZIP: 20005
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/386,727
: FILING DATE:
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: HOBBS, ANN S.
: REGISTRATION NUMBER: 36,830
: REFERENCE/DOCKET NUMBER: 4130/206916
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 202-861-3000
: TELEFAX: 202-822-0944
: TELEX: 6714627 CUSH
: INFORMATION FOR SEQ ID NO: 8:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 866 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-386-727-8

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Query Match      5.9%; Score 117.5; DB 1; Length 866;
Best Local Similarity 21.9%; Pred. No. 0.0076;
Matches 90; Conservative 58; Mismatches 140; Indels 123; Gaps 24;

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QY 2 NETV---KYSEFLVILCLC---CLLSYVSI---EGHRRAPGESRRNP-REIITPK 48
D 99 NEKVTKGRYQMV--ALCNADGCTLSDKKEIYVADTDSHLAPLNA---PLQENKPYT 153
QY 49 ESGKTIIGIYPSWSYVNHNLK-DLNPNLNVVHMSFAKMDLS--YDSISYGS-PL 101
D 154 NKAGRVGAYVYVWGVYGRKFTVDKIPAKNLIHILYGFPTICGGNGINDSLKEISGF 213
QY 102 LFKSLGLEIYGLNEY-----FNDAMNLRKARPDIIIMLSLG 138
D 214 LORSAGREDFVSIHDPRAVAVMGOGNLTAPDEPKKGFNGMLMALKRANPKILPSVG 273
QY 139 GETY-HPSSFDALNAVER-IANLYDELG---FDGIDVYE-----PNSGFDGLNDE 186
D 274 GWTLSDPFFEFSDTKRDTFVASMKEYLOTWKFEDGVIDIDWFEFGGAGNPNLGPNDG- 332
QY 187 KADFFVQYVTKLREYMCDDKLISISQSSNGALSCIGFNDPKKICDD-EAPYNSKYFKNP 245
D 333 ---ATYVALMKEL-----RAMLDELEAETGRGY--- 357
QY 246 DYKRELLRAAQMASAG--ATYLMNNLKMIDWVFOFNTNSTDSTVMKELDYSAV 302
D 358 ---ELTSA---ISAGGKIAKVYQAAQYMDYIFLMSYDFSGAPD---LKNLAHQTNL 407
QY 303 YGKKYDVYIMMGFTLMPSTPPNPNDKMLVKSIGDFVXTENTLNKRDGFG 353
D 408 YASSWD-----PATKTY-TDKGVKALLGGV--TPGVVVVGAAMYG 445

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RESULT 9
US-08-600-452A-8
Sequence 8, Application US/08600452A
Patent No. 5985644
GENERAL INFORMATION:
APPLICANT: ROSEMAN, SAUL
APPLICANT: BASSLER, BONNIE
APPLICANT: KEYHANT, NEMAT O.
APPLICANT: CHITLARU, EDITH
APPLICANT: ROWE, CHRIS
APPLICANT: YU, CHARLES
TITLE OF INVENTION: BACTERIAL CATABOLISM OF CHITIN
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & RICHARDSON P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/600,452A
FILING DATE: 13-FEB-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Halle, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07662/005001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 678-5070
TELEFAX: (619) 678-5099
TELEX:
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 866 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-600-452A-8

Query Match 5.98; Score 117.5; DB 2; Length 866;
Best Local Similarity 21.98; Pred. No. 0.0076;
Matches 90; Conservative 58; Mismatches 140; Indels 123; Gaps 24;

QY 2 NFTV---KSFVLYICLC---CLSTVYSVI---EGHRRPGRSKNP-REITKTFK 48
DB 99 NFKVTVGGRQOMV--ALCVNADGTLSDKKEIYVADTDGSHLALNA---PLQENNKRYT 153
QY 49 ESKGKIIGYTPSWSVSNHNK-DLNPNLNVHMSFAKMDL-----YDSIESIVGS-PL 101
DB 154 NKAGKVVGAYVEMGVGKRFYTDKIPAKNLTHTLYGFTPGCGNGINDSLKISGSPEA 213
QY 102 LFKSLIGLEITIGNEY-----FNDANLTKRARPDIIMLSLG 138
DB 214 LQBSCHGREDFFKVIHDPMAVOMGCGNLTADEPYKGFENLMAKLANPNLKLPSVG 273
QY 139 GERY-HPSFSDALNAEK-IANLVDELG---FDGIDVDYE-----PNSGFGIANDKE 186
DB 274 GWLSPDFYFFSDKTKDTIVASMKELQTMKFFDGYDIDMEFPGGAGANNLGPNDG- 332
QY 187 KADFEVQYVTKREYMODKLISISQSSNGALSCIGFNDPKKICMD-EADYNSKYFNKP 245
DB 333 ---ATYVALMKE-----RAMLDELEATGROY----- 357
QY 246 DYKELLRAQOMASAG---AIIYIMNLKMDIMKVYQTFNYTSTSTSTVKELEYDSVAY 302

DB 358 ---ELTSA---ISAGDKRIAKVDYQAQYMDYIFLMSYDFSGAFD---LKNLAHQTNL 407
QY 303 YGKKYDYIIMGFTLMPSTPFPNDKMLVKSIGDFVTEKLNKRADFGG 353
DB 408 YASSWD-----PATKYT-TDKGVKALLGQV-TPEKVYVGAAMTG 445

RESULT 10
US-08-392-625-24
Sequence 24, Application US/08392625
Patent No. 5837485
GENERAL INFORMATION:
APPLICANT: Enlian, Karl-Dieter
APPLICANT: G tz, Friedrich
APPLICANT: Schnell, No. 5837485bert
APPLICANT: Augustin, Johannes
APPLICANT: Engelke, Gernar
APPLICANT: Rosenstein, Ralf
APPLICANT: Kaletta, Corina
APPLICANT: Klein, Cora
APPLICANT: Wieland, Bernd
APPLICANT: Kuppe, Thomas
APPLICANT: Jung, G nther
APPLICANT: Kellner, Roland
TITLE OF INVENTION: Biosynthetic Process For The Preparation
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/392,625
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/876,791
FILING DATE: 30-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 0652,0980002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2540
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 461 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-392-625-24

Query Match 5.68; Score 111; DB 2; Length 461;
Best Local Similarity 21.08; Pred. No. 0.013;
Matches 86; Conservative 50; Mismatches 125; Indels 148; Gaps 17;

QY 6 KYSFLVLCCLCL-----STYVSIEGHARRPGRSKNP-REITKTFKES 50
DB 3 KEKFEIYFLISLVFLQNEYAFGSSLEEDLSYSV-----EYDAKTFKES 48
QY 51 --GKGIIGY-----YPSWYSYHNLKDLNPNLN---VHMSFAKMDLSTY 90
DB 49 IKQNIETLTYIPELHTAQITRSKSLNLSIKSNKVKFVNPFCSTCVVEKSVK----- 102

QY 91 DSIESIVGSPLEFKSLIGLEYIGLNEYFNDAMNLR-----KARP-----IMLSL 137
Db 103 -----TGKNLNKK-----NGSHDLFDRQWDMRKITNEGSKYKLSPPKRAKVALYDS 150
QY 138 GGETYHPSFSDALNAVEKIANLVDELGPDGIDVD-----YE-----PN 176
Db 151 GVNSSH-----IDLKSIINKIVNEVPKNGRSGSENDESGKNFEEDKLNIGTLVAGOIGAN 205
QY 177 GSFDDLNDKEKADFVQVYTKLREYWCDDK-LISISQSSNGALS-----CIGFNDPKKI 229
Db 206 GNLKGVNPGVEEMNIVRVFSGSKSEMLVWSKGIIDAANDNDVINYSLGNYLKIDNKK 265
QY 230 CMDDE-APYNSKYFNKPDYKKELLRAAQAASAGAIYIMNNLKMDIMVFOVTENYNTST 288
Db 266 LRDDEKVDYA-----LQKAINYAQKKGSIVVAAGNDGINVKKEINKKRNL 314
QY 289 DSTVKELEYDSAYYKKYDYIIMGFTLMPSTPPNPDKMLYKSIDG 337
Db 315 NKTSTKRYVDS-----PANLNMMVTGVSIDD 340

RESULT 11
US-08-466-961A-24
; Sequence 24, Application US/08466961A
; Patent No. 5843709
; GENERAL INFORMATION:
; APPLICANT: Entlan, Karl-Dieter
; APPLICANT: Gtz, Friedrich
; APPLICANT: Schnell, No. 5843709bert
; APPLICANT: Augustin, Johannes
; APPLICANT: Engelke, German
; APPLICANT: Rosenstein, Ralf
; APPLICANT: Kaletta, Corlina
; APPLICANT: Klein, Cora
; APPLICANT: Wleland, Bernd
; APPLICANT: Kupke, Thomas
; APPLICANT: Jung, G. nther
; APPLICANT: Kellner, Roland
; TITLE OF INVENTION: Biosynthetic Process for the Preparation of
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, NW
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,961A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/392,625
; FILING DATE: 22-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/876,791
; FILING DATE: 30-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/784,234
; FILING DATE: 31-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 0652-0980004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540

; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 461 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-466-961A-24

Query Match 5.6%; Score 111; DB 2; Length 461;
Best Local Similarity 21.0%; Pred. No. 0.013;
Matches 86; Conservative 50; Mismatches 125; Indels 148; Gaps 17;

QY 6 KTSFLVLCILCLL-----STYVSVEGHRARPGESKKNPRETIKTFKS 50
Db 3 KKEFFIVFLILSVLFONEYARGSSLNEELSYYSV-----EYDNAKTFKS 48
QY 51 --GKGIIQY-----YPSWVSYNHLLKDLNPLN--VYHMSPAKMDLSY 90
Db 49 IKQKIELTYKIPELHTAOKTSKSLNLSKNKVKFVNPICSTCYVEKSYK----- 102
QY 91 DSIESIVGSPLEFKSLIGLEYIGLNEYFNDAMNLR-----KARP-----IMLSL 137
Db 103 -----TGKNLNKK-----NGSHDLFDRQWDMRKITNEGSKYKLSPPKRAKVALYDS 150
QY 138 GGETYHPSFSDALNAVEKIANLVDELGPDGIDVD-----YE-----PN 176
Db 151 GVNSSH-----IDLKSIINKIVNEVPKNGRSGSENDESGKNFEEDKLNIGTLVAGOIGAN 205
QY 177 GSFDDLNDKEKADFVQVYTKLREYWCDDK-LISISQSSNGALS-----CIGFNDPKKI 229
Db 206 GNLKGVNPGVEEMNIVRVFSGSKSEMLVWSKGIIDAANDNDVINYSLGNYLKIDNKK 265
QY 230 CMDDE-APYNSKYFNKPDYKKELLRAAQAASAGAIYIMNNLKMDIMVFOVTENYNTST 288
Db 266 LRDDEKVDYA-----LQKAINYAQKKGSIVVAAGNDGINVKKEINKKRNL 314
QY 289 DSTVKELEYDSAYYKKYDYIIMGFTLMPSTPPNPDKMLYKSIDG 337
Db 315 NKTSTKRYVDS-----PANLNMMVTGVSIDD 340

RESULT 12
US-08-645-193B-26
; Sequence 26, Application US/08645193B
; Patent No. 5962253
; GENERAL INFORMATION:
; APPLICANT: Kupke, Thomas
; APPLICANT: Gutz, Friedrich
; APPLICANT: Kemper, Christoph
; APPLICANT: Jung, Gunther
; TITLE OF INVENTION: Oxidative Decarboxylation of Peptides
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/645,193B
; FILING DATE: 13-MAY-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 0652.1540000

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 371-2600
 TELEFAX: (202) 371-2540
 INFORMATION FOR SEQ ID NO: 26:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 461 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: not relevant
 MOLECULE TYPE: protein
 US-08-645-193B-26

Query Match 5.6%; Score 111; DB 2; Length 461;
 Best Local Similarity 21.0%; Pred. No. 0.013;
 Matches 86; Conservative 50; Mismatches 125; Indels 148; Gaps 17;

QY 6 KYFVLVLCCLL-----STYVYIEGHRARPGESKRNPREIITKTES 50
 DB 3 KKEFFVFLILVFLQNEKAFGSSLNDELSTYSV-----EYDNKTFKES 48
 QY 51 --GKGIIGY-----YPSWYSYNNLKDLPNLN--VYHMSFAMDLSTY 90
 DB 49 IKKNIEELTYKIPELHQAQIKTSKSLNLIKSKKNKVFVNPCTCYEKSVK----- 102
 QY 91 DSIESIVGSPFLFKSLIGLEYIGLNEYFNDAMLR-----KARPD---IIMLSL 137
 DB 103 -----TGKMLNNKK-----NGSHDLFDROMDKRITNECKSYKLPDRKKAKVALVDS 150
 QY 138 GGFYHPSFDSALNAYEKILANLYDELGFQIDVD-----YE-----PN 176
 DB 151 GVNSH-----TDLKSTNKTYNEVPKNGFSGNDESGNKNFEEDKLNHGLVLAQIGAN 205
 QY 177 GSPDGLNDEKADFEVQYVTKLREYMCDDK-LISISOSNGALS-----CIGFNDPKI 229
 DB 206 GNLKYNPGEVMYRYRFGSKSEMLWVSGIIDAANDNDVIVSLGNLYIKNOKKK 265
 QY 230 CMDEAPYNSKYFNKDYKKEILRAAOMASAGALYILMNNLKIMDMVYQTFNYTNT 288
 DB 266 LRDEVDYDA-----LQKAINYAOKKGIYAAVANGINGINKKKEIKKNNL 314
 QY 289 DSTVMEKELYSAAYGKKDYVILMFTLPSTPFPNDKMLKYSIGD 337
 DB 315 NSKTSKVIDS-----PAILNNMIVGSIID 340

RESULT 13
 US-09-025-691-3
 Sequence 3, Application US/09025691
 Patent No. 6069299
 GENERAL INFORMATION:
 APPLICANT: Broadway, Roxanne M.
 APPLICANT: Harman, Gary E.
 TITLE OF INVENTION: FUNGUS AND INSECT CONTROL WITH
 TITLE OF INVENTION: CHITINOLYTIC ENZYMES
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
 STREET: Clinton Square, P.O. Box 1051
 CITY: Rochester
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 14603
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/025,691
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:

NAME: Goldman, Michael L.
 REGISTRATION NUMBER: 30,727
 REFERENCE/DOCKET NUMBER: 19603/20120
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (716) 263-1304
 TELEFAX: (716) 263-1600
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 376 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-025-691-3

Query Match 5.6%; Score 110.5; DB 3; Length 376;
 Best Local Similarity 22.3%; Pred. No. 0.01;
 Matches 68; Conservative 28; Mismatches 84; Indels 125; Gaps 15;

QY 33 PGEKRNPREIITKTESGKGIIGYYPWSY--NNLKDLP--NPNLNVHM----- 81
 DB 2 PG-----PGREKINL-----GYTEMGVYGRNHYKNNLYTSGSAEKITHINISFGN 48
 QY 82 -----SFAKMDLSYDIESIVG-----SPLLFKSLIGLEYIGLNEYFNDAMLR 125
 DB 49 VQGGKCTIGDSFAAYDKAYTAESVDGADTWDQ-----LRGNFNQLRKLK 95
 QY 126 KARDIIMLSLGEYTHPSFDSALN---VEKIANLYDELG---FDGIDVYE--PN- 176
 DB 96 AKYPIKILWSEFGMTWSSGFTDAVKNPAPAFKSCDLVEDPRADYFDSIDIDMEYFPA 155
 QY 177 -----GSPDGLNDEKADFEVQYVTKLREYMCDDK-LISISOSNGALS-CIGFNDP 226
 DB 156 GGLSDSSGPAALKNMVAQMRAGFTDLYT-----AATFADASSGKL----- 198
 QY 227 KKTICMDEAPYNSKYFNKDYKKEILRAAOMASAGALYILMNNLKIMDMVYQTFNYT 286
 DB 199 -----DAADY-----AGAAQY-----FDWYNVMTYDFEG 222
 QY 287 STDST 291
 DB 223 AMDKT 227

RESULT 14
 US-08-308-872B-6
 Sequence 6, Application US/08308872B
 Patent No. 5661006
 GENERAL INFORMATION:
 APPLICANT: BROWN, Thomas David Kay
 APPLICANT: HORSBURGH, Brian Colin
 TITLE OF INVENTION: CANINE CORONAVIRUS SUBUNIT VACCINE
 NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Akzo No. 5661006el Patent Department
 STREET: 1300 Piccard Drive, Suite 206
 CITY: Rockville
 STATE: Maryland
 COUNTRY: U.S.A.
 ZIP: 20850
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/308,872B
 FILING DATE: 19-SEP-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/042,846
 FILING DATE: 05-APR-1993
 PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/872,641
FILING DATE: 24-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 91.303.737.0
FILING DATE: 25-APR-1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gormley, Mary E.
REGISTRATION NUMBER: 34,409
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 258-5200
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1453 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Canine corona virus
STRAIN: CCV-C54
FEATURE:
NAME/KEY: Protein
LOCATION: 1..1453
OTHER INFORMATION: /label= CCV-C54_spike
US-08-308-872B-6

Query Match 5.5%; Score 108.5; DB 1; Length 1453;
Best Local Similarity 20.9%; Pred. No. 0.13; Indels 111; Gaps 17;
Matches 78; Conservative 43; Mismatches 141;

QY 10 LVICLLCCLSTVYSVI-----EGHRAPEGSESRKNPREIITKFEKSGKIIOGYYP 60
DB 1 MVLTLCLLPSYNSVICTSNNDQVAVTQLPGNENIKDFLQNFKEEGSVVVGYYP 60
QY 61 SWVSN-----NHLKDLNPNLVNHSFAKMDISYSIESIVSPLIFK----- 104
DB 61 TEVWNCSTRATTTAYHFSN-----IHAFFYEDMEAMNSTGNARCKPLLVHVGSPV 113
QY 105 SLIGLEYIGLMEYFNDAMNLRKRPDIIMLSIG-----GETYAPSSPDSA-----LN 152
DB 114 SIT-----VYSAIKDDVON---RP---LKHGLICTTKNSTIDYNSFTSQWFDICLG 161
QY 153 AVERIANLVDELGFDGIDVDEPNGS--FDGLNDEKADFFVOYVTKLEVMODKLIS 211
DB 162 TDRKIP-----FSVYPTD---NGTKLEGL-----EMTDDVYV---AYISDD-----S 197
QY 212 QSSNGALSCIGFNDPKKICMDDEAPYNSKYFNKPDVKELLRQAQMASAGAI----- 264
DB 198 HRLN-----INTNMFNNVTIILYRSSTATWOKSAAYVVOGVSNF 236
QY 265 --YLMNNLKDMDVFOYFNTNSTDSTVMKELYDVAAYGKKYDYIINGFTLMPST 322
DB 237 TYKLTNNTNGLAKSYELCDIEYCTGATNVPAPISGCIIPDGFSENNFMILNISTFVSG 296
QY 323 PFNPDKMLVXSI 335
DB 297 RFTVNQPLLVNCL 309

RESULT 15
US-08-524-051-2
Sequence 2, Application US/08524051
Patent No. 5866788
GENERAL INFORMATION:
APPLICANT: Kramer, Karl J.
APPLICANT: Muthukrishnan, Subbaratnam
APPLICANT: Choi, Hee Kyung
APPLICANT: Corpuz, Lolita
APPLICANT: Gopalakrishnan, Bhuvana
TITLE OF INVENTION: RECOMBINANT CHITINASE AND USE THEREOF AS
TITLE OF INVENTION: A BIOCID

NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hovey, Williams, Timmons & Collins
STREET: 2405 Grand Blvd., Suite 400
CITY: Kansas City
STATE: MO
COUNTRY: USA
ZIP: 64108
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/524,051
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Collins, John M.
REGISTRATION NUMBER: 26,262
REFERENCE/DOCKET NUMBER: 22875-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (816)474-9050
TELEFAX: (816)474-9057
TELEX: 434-363
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 554 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-524-051-2

Query Match 5.4%; Score 107; DB 2; Length 554;
Best Local Similarity 20.4%; Pred. No. 0.041; Indels 28; Gaps 6;
Matches 32; Conservative 40; Mismatches 57;

QY 58 YPSPVWSY-----NHLKDLNPNLVNHSFAKMDLSYDSIESIVSPLIFKSLGLEXY 112
DB 28 YFSNNAVYRPGVGRYCIIDI--PVEKCTHIYISFICVTGNSVLLIIDELVDKNG---- 82
QY 113 GLNEYFNDAMNLRKRPDIIMLSIGGETYHPSSF-----DSLNAVEKIANLVDELG 165
DB 83 -----FRNFTSLRSHSPSVKFAVAGWAGSSKYSHWAAKSTMSFIRSVSFLKYYD 137
QY 166 FDGIDVDYDEPNGSFD---GLNDEKADFFVOYVTKLR 199
DB 138 FDGLDMDIEYFGADRGGSFSBCKR---FLYLVQELR 171

Search completed: May 8, 2002, 08:57:29
Job time: 22 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 8, 2002, 08:57:07 ; Search time 15.99 seconds
(without alignments)
1800.749 Million cell updates/sec

Title: US-09-579-383-3

Perfect score: 1982

Sequence: 1 MNETYKYSFLVTCILLCCLLS.....SDNAHNEQLATEYFVESLH 378

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 segs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR_68:*

1: PIR1:.*
2: PIR2:.*
3: PIR3:.*
4: PIR4:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	169.5	8.6	699	2	A38368 chitinase (EC 3.2.
2	146.5	7.4	1088	2	D82246 probable chitinase
3	140.5	7.1	610	2	JH0573 chitinase (EC 3.2.
4	139	7.0	427	2	JC4565 chitinase (EC 3.2.
5	136	6.9	274	2	JW0077 chitinase (EC 3.2.
6	132.5	6.7	599	2	D83764 chitinase BH0916 [
7	130.5	6.6	423	2	S51369 chitinase - fungus
8	127.5	6.4	561	2	A25090 chitinase (EC 3.2.
9	126.5	6.4	563	2	S60651 chitinase precursor
10	126.5	6.4	609	2	T42073 probable chitinase
11	126.5	6.4	1054	2	T30933 chitinase (EC 3.2.
12	124.5	6.3	511	2	S61166 probable membrane
13	123.5	6.2	417	2	T42074 chitinase
14	122	6.2	291	2	S56698 chitinase
15	121	6.1	285	2	S49898 chitinase (EC 3.2.
16	120.5	6.1	424	2	S47133 chitinase (EC 3.2.
17	119.5	6.0	831	2	T00333 chitinase (EC 3.2.
18	119	6.0	466	2	T28216 chitinase (EC 3.2.
19	119	6.0	558	2	T30418 chitinase (EC 3.2.
20	117	5.9	276	2	S56696 chitinase (EC 3.2.
21	116	5.9	291	2	S56697 chitinase (EC 3.2.
22	115.5	5.8	504	2	A38221 chitinase (EC 3.2.
23	114.5	5.7	413	2	JC2135 chitinase (EC 3.2.
24	113	5.7	1213	2	T43916 chitinase A [impor
25	112.5	5.7	571	1	JN0858 chitinase (EC 3.2.
26	112.5	5.7	571	1	T42071 probable chitinase
27	112.5	5.7	668	2	D70129 chitinase (EC 3.2.
28	112.5	5.7	1051	2	D82428 chitinase (EC 3.2.
29	112	5.7	492	2	F86868 chitinase (EC 3.2.

30	111	5.6	285	2	S49879 hypothetical narbo
31	111	5.6	461	2	S23420 probable subtilisi
32	110.5	5.6	349	2	D70103 hypothetical prote
33	110.5	5.6	546	2	F84238 chitinase [impor
34	110	5.5	285	2	T12157 nodulin - fava bea
35	110	5.5	544	2	G64483 hypothetical prote
36	109.5	5.5	424	2	S68121 chitinase I precu
37	109.5	5.5	846	2	C82135 chitinase VC1952 [
38	107	5.4	554	2	A56596 chitinase (EC 3.2.
39	107	5.4	758	2	S37855 hypothetical prote
40	107	5.4	975	2	T08606 protein phosphatas
41	106.5	5.4	552	2	T41863 chitinase chl-A or
42	106	5.3	285	2	S49880 hypothetical narbo
43	105.5	5.3	736	2	B82944 ribose/galactose A
44	105	5.3	275	2	JE0184 chitinase (EC 3.2.
45	105	5.3	441	2	D83555 hypothetical prote

ALIGNMENTS

Query Match	8.6%	Score 169.5	DB 2	Length 699
Best local similarity	20.0%	Pred. No. 0.00028		
Matches	88	Conservative	58	Mismatches 113; Indels 181; Gaps 21
QY	55	IQGYPSWVSY--NNLKDLPNPNLVHMSFAKMDLSYDSIES-----	95	
DB	46	IVGYPSMAVGRNVADIDPT-KVTHINAFADICWNGHGNPDSPGNPVWTQNE	104	
QY	96	-----IVGSPLEFKSLGLEIYG-----LNEYFDAMNLRKRPDIIMLSL	137	
DB	105	KSQITVNPNGTIVLDPMID--TGKTFAGDTWDQPIAGNINQLKLTQTNPNLTIISV	161	
QY	138	GGETYHPSPFSALNAV--EKIAN-LVDEL--GPDGIDVDE--PNSFQDLNKEKAD	189	
DB	162	GGWTSNRPSDVAATPAAREVFANSAVDPLRKYNFDGVDLMEYVSGGLD--NSKRPED	220	
QY	190	--FFQVYTKLEHYKCDPKLISISQSSNGALSCIGFNDPKKICMDDEAPYNSKYRNKPDY	247	
DB	221	KONYTLILSKIREKL-----DAAGAV-----	243	
QY	248	KKELIRAAOMASAGAITLMN---NLKMDIDMVFVQTFNTNSTDSIVYMKEL---	300	
DB	244	KKYLL--TIASGASATYAANTELAKIAIYDWMIMMYDFGAWQKISAHNAPLNYDPA	300	
QY	301	A--	308	
DB	301	ASAGVDPANTFNVAAGQCHLDAGVPAKLVLYGPFYGRGWDGCAQAGNGOYOTCTGGS	360	
QY	309	-----YVIMGFTELPSPSP-----FNPDKMLV-----KSYGDEVK	340	
DB	361	SVGTWEAGSPFDYDEANVYINKNGYTRWMDPAKVPYLYNMSNKRFFISYDAESVG--YK	418	
QY	341	TENKLNKRADGGLWMSLSSD	360	

Db 419 TAYIKSKGLGAMFWEISGD 438

RESULT 2

D82246
probable chitinase VC1073 (imported) - Vibrio cholerae (strain N16961 serogroup O1)
C:Species: Vibrio cholerae
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C:Accession: D82246
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bress, S.; Qin, H.; Dragol, I.; Sellers, H.
1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: A82035; MUID:20406833
A:Accession: D82246
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-1088 <HE1>
A:Cross-references: GB:AE004188; GB:AE003852; NID:9655530; PIDN:AAF94232.1; GSPDB:GN001
C:Genetics: serogroup O1; strain N16961; biotype El Tor
A:Gene: VC1073
A:Map position: 1

Query Match 7.4%; Score 146.5; DB 2; Length 1088;
Best Local Similarity 23.6%; Pred. No. 0.021; Mismatches 103; Indels 93; Gaps 21;
Matches 79; Conservative 60; Mismatches 103; Indels 93; Gaps 21;

Qy 39 NPREIITFKESGKGIIOGYPSWVSYNHNLK-----DLNPLNVNHSFA-----KMDL 88
Db 383 HPRRLI-----GYTSMRTGKNGLPAYLAGDL-FMEKTLTHINYPASINKDOF 429
Qy 89 SYSTESIVSPLFKSLIGLE-----YIGLNEFNDAMLRKRPDIIMLSIGG--E 140
Db 430 SMOVDSD--ATKMTWENVGAEKMPSLPYQG--HFNLSEFKQYPPVKTLISVGWAE 484
Qy 141 T--YHPSSPSFA-----LNAVEKTA-NLYDELGPDGIVDYE-PNGSPDGLDKRKA 188
Db 485 TGGFYPTTDLASCYSVMEGKAFNKSADVDFIRQDFGVDIDIEYPSMKDSGN---PV 541
Qy 189 DFEVQVYTKLREYKCDKLISISOSNGALSCIGFNDPKKICMDDEAFYNSKYENKPPVK 248
Db 542 DF--EQSNGKRCGQLMDVNYMMTELK-ALDKAGEGDRRRMLTASP--SSAY----- 590
Qy 249 KELLRAAQMASAGAITLNNLKDMDVYQTFN-----YTNSDSTVM 293
Db 591 --LIRGMQDEFA-----MDVLDVYVNIIMSYDLHGTWNEFVGPOALFPDDKDAELA 638
Qy 294 K-ELYDSYAYGKKYDVYIIMGFTLMPSPSTPPFN 327
Db 639 KMGVYTTAEYQIGY---LNOAMTHHFFRCAFKPS 670

RESULT 3

JH0573
chitinase (EC 3.2.1.14) 63 - Streptomyces plicatus
C:Species: Streptomyces plicatus
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 31-Mar-2000
C:Accession: JH0573; A29912
R:Robbins, P.W.; Overbye, K.; Albright, C.; Benfield, B.; Pero, J.
Gene 111, 69-76, 1992
A:Title: Cloning and high-level expression of chitinase-encoding gene of Streptomyces p.
A:Reference number: JH0573; MUID:92192480
A:Accession: JH0573
A:Molecule type: DNA
A:Residues: 1-610 <ROB>
A:Cross-references: GB:M82804; NID:q153215; PIDN:AAA26720.1; PID:q153216
A:Note: the authors translated the codon AAG for residue 360, 406, 431, 442, 460, 489, 4
J. Biol. Chem. 263, 443-447, 1988

A:Title: Cloning and expression of a Streptomyces plicatus chitinase (chitinase-63) 1
A:Reference number: A29912; MUID:88087127
A:Accession: A29912
A:Molecule type: DNA
A:Residues: 1-2, '1', 4-45 <RO2>
A:Cross-references: GB:M18397; NID:q153208; PIDN:AAA26717.1; PID:q153209
C:Comment: This protein is related with the steps in chitin utilization.
C:Genetics:
A:Gene: chta
C:Superfamily: Streptomyces plicatus chitinase 63; bacterial cellulose-binding domain
C:Keywords: glycosidase; hydrolase; polysaccharide degradation
F:33-132/Domain: Bacterial cellulose-binding domain homology <BCB>

Query Match 7.1%; Score 140.5; DB 2; Length 610;
Best Local Similarity 21.4%; Pred. No. 0.026; Mismatches 108; Indels 131; Gaps 17;
Matches 79; Conservative 51; Mismatches 108; Indels 131; Gaps 17;

Qy 34 GESRRNPREIITFKESGKGIIOGYPSWVSY--NHNKDL-----NPNLN--- 77
Db 232 GEPNPNP-----GAEYKMGYFTWVGYYGRNHYHVKNLVTSASAKITHINLRFQNV 281
Qy 78 -----VYMSFAKMDLSDSIESIVG-----SPLFKSLIGLEYIGLNEFNDAMLRK 126
Db 282 QGKCTIDDAAYADYKATYADQSVDGADYWDQ-----LRANFQRLKLA 328
Qy 127 ARPDIMLSIGERY-----HPSSFDALNAVEKIANLYDELGPDGIVDYE-PN 176
Db 329 EYPIHKLILYSFGWTWSGCFPDAYKKNPAFAKSGHDLVEDPRMADY--FGIDIDMEYRN 366
Qy 177 GSFDDLNDKEKADFEVQVYTKLREYKCDKLISISOSNGALSCIGFNDPKKICMDDEAP 236
Db 387 AGLSCDETSAPNAPFSSMKAMRAEFQGDYLTITAAVADG-----SDGKI---DAAD 436
Qy 237 YN--SKYFNKPDYKELLRAAQMASAGAITLNNLKDMDVYQTFNNTNSDSTVM 294
Db 437 YGEASKY-----IDVYVMTYD----- 454
Qy 295 ELYDSYAYG-----KKYDVYIIMGFTLMPSPSTPPN-----PNDKMLVKSIGDFYKTE 342
Db 455 --FGAMAKNGPAPHPSPINATYDGIQOGFTTADAMAFKSKGVADRLLI-GIGFYRGW 511
Qy 343 NKLNRADG 351
Db 512 TGVYQSAPG 520

RESULT 4

JC4565
chitinase (EC 3.2.1.14) 1 precursor - Coccidioides immitis
N:Alternate names: complement fixation antigen homolog; CT51 protein
C:Species: Coccidioides immitis
C:Date: 12-Mar-1996 #sequence_revision 19-Apr-1996 #text_change 13-Nov-1998
C:Accession: JC4565
R:Pishko, E.J.; Kirkland, T.N.; Cole, G.T.
Gene 167, 173-177, 1995
A:Title: Isolation and characterization of two chitinase-encoding genes (ctsl, ctst2)
A:Reference number: JC4565; MUID:96144270
A:Accession: JC4565
A:Molecule type: mRNA
A:Residues: 1-427 <PIS>
A:Cross-references: GB:L41663
A:Experimental source: C735
C:Genetics:
A:Gene: ctst1
A:Introns: 47/3; 171/3; 191/3; 215/2; 391/3
C:Superfamily: Streptomyces chitinase ch140
C:Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-427/Product: chitinase 1 #status predicted <MAT>
F:387/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 7.0%; Score 139; DB 2; Length 427;
 Best Local Similarity 23.7%; Pred. No. 0.021;
 Matches 89; Conservative 55; Mismatches 118; Indels 114; Gaps 21;

OY 9 FLVCLLCCLLSTYVSVIEGHRARGESKRNREIIKFKESG-KGIIGGYPSWVS-- 65
 DB 3 FLIGALL--TLQTLV-----OASSMSMPNSYPVEAPAEKGFSVY--YVWNAIYGR 52
 OY 66 NNNLKDLNPLNVVHMSFA-----KMDLSYDSIESIVGSPFLFKSLGLEIGL 114
 DB 53 GNNPDQLKAD-QFHILIVAFANIRSGEYVLDTWADTKKHFGDK-----MDERPN 103
 OY 115 NEY--FNDAMLRKARPDIIIMLSIGETYPSPSSDALNAVE---KIAN---LVDELG 165
 DB 104 NYGCGIKQWYLLKKNRNKTLTLISIGWYSP-NFKTPASTEGRKKFADTSLKIMKDG 162
 OY 166 FPGIDVDE-PNGSPDGLNDKEKADFEVQYVTKREYMDOKLISISQSNALSCIGN 224
 DB 163 FPGIDWDEY-----EDERQANDFVLL----- 186
 OY 225 DPKKICMDDEAFYNSKYFNKPDVKELRAAOMASAGAIYLMNMLKDM---IDWVYQV 281
 DB 187 ---KACREALDAYSAKH---FNGKKFLTLTA--SPAGQNYNKLKLAEMDKYLDPMNLMA 238
 OY 282 FNYTSTD--STVMEKYDYSAVYGGKYDYIIMGFTLMFPSTPPNPKMLVKSIGDFV 339
 DB 239 YDFSGSMDKVSCHMSNVPS-----TTKPESTPFSSD-----KAVKDYI 277
 OY 340 KTEENKLRKADGFLM 355
 DB 278 KAGVPANKIVLGMPLY 293

RESULT 5

chitinase (EC 3.2.1.14) a - Gladiolus gandavensis
 C:Species: Gladiolus gandavensis
 C:Date: 17-Jun-1998 #sequence_revision 10-Jul-1998 #text_change 07-May-1999
 C:Accession: J00077
 R:Yamagami, T.; Mine, Y.; Ishiguro, M.
 Biosci. Biotechnol. Biochem. 62, 386-389, 1998
 A:Title: Complete amino acid sequence of chitinase-a from bulbs of gladiolus (Gladiolus
 A:Reference number: J00077; MUID:98193995
 A:Accession: J00077
 A:Molecule type: protein
 A:Residues: 1-274 <YAM>
 A:Experimental source: bulbs
 C:Comment: This enzyme hydrolyzes beta-1,4-linked N-acetylglucosamine polymer chitin.
 C:Superfamily: alcohol sulfotransferase
 C:Keywords: glycosidase; hydrolase

Query Match 6.9%; Score 136; DB 2; Length 274;
 Best Local Similarity 22.4%; Pred. No. 0.019;
 Matches 74; Conservative 49; Mismatches 102; Indels 106; Gaps 16;

OY 72 LNPINLVH--MSFAKMDLSYDSIESIVGSPFLFKSLGLEIGLNEYFN--DAMNLRK 126
 DB 21 INPRITDFQVLSFA-----IDYVSTP-----HTPTNGKFNWMDSSNLGP 62
 OY 127 ARPDII-----MLSLGET-----YHSSFDNAL-NAVEKIANLVDELGFDGID 170
 DB 63 SOVDIKSHNNVRAVSLGATVGKSVQVQPSIDSMWNAVSSLQIIDRYMLDGD 122
 OY 171 VDYEFGSFDGLNDEKEDFEVQYVTKREYMDOKLISISQSNALSCIGFNDPKKIC 230
 DB 123 IDYENFOYTD-----PDTRAECTIGRLITLTKRRNVINFSI----- 158
 OY 231 MDDEAPYNSKYFNKPDVKELRAAOMASAGAIYLMNMLKDMIDWVQGFNYTNSDS 290
 DB 159 ---APF-----PDVEEYLA-----LMNRKYVNIHINQFAYADSSSTTV 195
 OY 291 TVMKELYSYA--YIGKRYDYIIMGFTLMFPSTPPNPKMLVKSIGD---FVTEENKL 345

DB 196 RQFLKXYDPAVSKYRG-----GNVLISFSTERDAGLTVDRGFPAASILKROKRL 246
 OY 346 NKRADGFLMS--LSSDNAHNEOLAIEYFV 374
 DB 247 H-----GIAVMSADTSKSNGRFIDEAOSFLV 273

RESULT 6

chitinase BH0916 [imported] - Bacillus halodurans (strain C-125)
 C:Species: Bacillus halodurans
 C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 31-Dec-2000
 C:Accession: D83764
 R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; H
 Nucleic Acids Res. 28, 4317-4331, 2000
 A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a
 A:Reference number: AB3650; MUID:20263314
 A:Accession: D83764
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-599 <STO>
 A:Cross-references: GB:AP001510; GB:BA000004; NID:q10173440; PIDN:BAB04635.1; GSPDB:G
 C:Genetics:
 A:Gene: BH0916

Query Match 6.7%; Score 132.5; DB 2; Length 599;
 Best Local Similarity 22.2%; Pred. No. 0.094;
 Matches 62; Conservative 42; Mismatches 82; Indels 93; Gaps 13;

OY 55 IOGYPPSWVS--NNMLKDLNPLNVHMSFAKMDLSYDSIES----- 95
 DB 42 IVAYYPSMGAYGRDYQVMDIDAS-KISHINVAFANICMDGRHGNPDPAQNPQTWCSO 100
 OY 96 -----IVGSPFL--FKSLGLEI-IGLNEYFNDAAMLRKARPDIIIMLSIGET 141
 DB 101 NGVIDVPGNSIYMGDPWIDAOKSNPGDTWDEPLRGNFKOLNKTKEHPHLKTLISVGGWT 160
 OY 142 YHSSFDNAL--NAVEKIANLVDELGFDGIDVDE--PNGSPDGLN---DKEKAD 189
 DB 161 WSNRSDMAATETRNPNFANSVEFTRKYGFDGVYDWMYPSGGLPGNSRREDKENNY 220
 OY 190 FFEVQYVTKREYMDOKLISISQSNALSCIGFNDPKKICMDDEAFYNSKYFNKPDVK 249
 DB 221 LLLQEV-----DKL-----DEA-----GQEDGRD 240
 OY 250 ELLRAAOMASAGAIYLMN-----LKDMIDWVQGFNY 284
 DB 241 YLLTIASGASPG---YVENNKLMELAEIVDWIMIMTYDF 276

RESULT 7

chitinase - fungus (Trichoderma harzianum)
 C:Species: Trichoderma harzianum
 C:Date: 15-Jul-1995 #sequence_revision 19-Apr-1996 #text_change 28-May-1999
 C:Accession: S51369
 R:Garcia, I.; Lora, J.M.; de la Cruz, J.; Benitez, T.; Lobell, A.; Plincor-Toro, J.A.
 Curr. Genet. 27, 83-89, 1994
 A:Title: Cloning and characterization of a chitinase (CHT42) cDNA from the mycoparas
 A:Reference number: S51369; MUID:95269313
 A:Accession: S51369
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-423 <GAR>
 A:Cross-references: GB:S78423; NID:g999375; PIDN:AAB34355.1; PID:g999376
 C:Superfamily: Streptomyces chitinase chl40

Query Match 6.6%; Score 130.5; DB 2; Length 423;
 Best Local Similarity 21.6%; Pred. No. 0.083;

Best Local Similarity 20.7%; Pred. No. 0.26;
Matches 73; Conservative 54; Mismatches 105; Indels 121; Gaps 16;

```
OY 50 SSGKIIIGIYPSWVST--NHNLIKDLNPIN---VYHM-----SFAKMDL 88
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 237 TGAEYKMGGYFTNMWGYGRNVHVKNLVTSGSADKITHINAFNGVGGKCTIGDSYADYDK 296
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 89 SYDSTESIY-----SPLLFKSLGLEIYIGLNEYFNAMNLRKARPDITMISLGGFTY 142
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 297 ATTAADOSVVGADYDTWDQ-----LRGNFNOLRKIKAKYPTKILYSFGMTW 343
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 143 -----HPSSFSALNAVERKIANLYDELGFDSIDVYE--PNSGFDGLANDKERADFFV 192
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 344 SGGFPDVAVKNPAPAFKSCHDILVEDPRMADY--FDGIDLDMEYFNACGSDETSAPNAFS 401
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 193 QYVTLREHMCDDKLISISOSSNGALSCIGFNDPRKKICMDDEAPIN--SKYNNKDYVKE 250
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 402 SMKAKMRFEFGDYLITAAVTADG-----SDGKTI--DAADYGEASKY----- 442
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 251 ILRAQAQMASAGAIYILMNLIKDMIDMVEVQEPENYNSTSDTSYMKELYSAYYG----- 304
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 443 -----IDWYNMTYDF-----FGAMANGFTAPHS 467
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 305 --KRTDYIYIMFTLMPSTPPN---PNCKMLVKSIGDFYKTEKKLNKRADG 351
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 468 PLTAADGIPQOGFNTADAMAKFKSGVPADKLLI-GIGFYGRGTGVTYQSAPG 519
```

RESULT 11
T30933
chitinase (EC 3.2.1.14) A - Pseudoalteromonas sp. (strain S9)
C:Species: Pseudoalteromonas sp.
A:Variety: strain S9
C:Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 02-Sep-2000
C:Accession: T30933
R:Techkarnjanaruk, S.; Goodman, A.E.
Microbiology 145, 925-934, 1999
A:Title: Multiple genes involved in chitin degradation from the marine bacterium *Pseudoc*
A:Reference number: Z20935; MUID:99235578
A:Accession: T30933
A:Status: Preliminary; translated from GR/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1054 <TEC>
A:Cross-references: EMBL:AF007894; NID:g3928771; PID:g3928775; PIDN:AACT9665.1
C:Genetics:
A:Gene: chitA
:keywords: glycosidase; hydrolase

	Query Match	6.4%	Score 126.5;	DB 2;	Length 1054;
	Best Local Similarity	20.4%;	Pred. No. 0.55;		
	Matches 79;	Conservative 42;	Mismatches 85;	Indels 181;	Gaps 19;
Qy	NPRELIITFKKSGKGIIGYYPW-----VSYHNKLKDLNPLNVVHMSRAKKDLSYD	91			
Dd	318 HPRRYI-----GYFTSWRNNGANGOPSY---LVDDIPMDKIYHINFAFAYDAN	362			
Qy	92 SIESI-----VGSP--LLFKSLGLE-----YIGLNEYFDAMNLKRARDIMLSL	137			
Dd	363 NKVSIGDSGAAGNPAATNMENMPGVACAEKMDPTLPYKG---HRLNLKYKKLHPDYKTLLSV	419			
Qy	138 GGETYHPSSFD-----SALNAVEKIA-NLVDELGEFGIDVD	172			
Dd	420 GGMASETGTFPDANGNRVASGGFYTMNTNADGSVMYNAGINAFKSAVERIETIYGFPGVID	479			
Qy	173 YEPNGSEFGLANDKEADFVOIVTKLRREYMCDDKLISISQSSNGALSCTGFNDPKKICMD	232			
Dd	480 YEYPS--MNDSCHPDDF-----PISNARRA-----GINASYOVLN-	513			
Qy	233 DEAPYSKYFPNKRPDKRLLRAQMA-----SAGAIIYIMNNLKLMIDMVFOYT	281			
Dd	514 -----KITLRRELDKAGELAGKHMYLTASPSSG---YLIRGM-----ET	549			

```
QY      282 ENYTSSTSTSVKVELDYSAVYGKKRVDYIIIMGFTLHSPFRPNDRMKLVYSIGDPVKT   341
          |         |         |         |         |         |         |
Db       550 PQTT-----KLDYVNINISYL-----566

QY      342 ENKLNRADFGISSLSDNMAHNQQL    368
          |         |         |         |
Db       567 -----HGAW--NDHVGHNAAL    580
```

```

RESULT      12
S61166
probable membrane protein YDR371w - yeast (Saccharomyces cerevisiae)
N.Alternate names: hypothetical protein D9481.7
C.Species: Saccharomyces cerevisiae
C.Date: 23-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 17-Mar-2000
C.Accession: S61166
R.Ding, H.
submitted to the EMBL Data Library, June 1995
A.Description: The sequence of S. cerevisiae cosmid 9481.
A.Reference number: S61159
A.Accession: S61166
A.Molecule type: DNA
A.Residues: 1-511 <DIN>
A.Cross-references: EMBL:U28373; NTD:g849184; PID:g849192; GSPDB:GN000004; MIPS:YDR371
A.Experimental source: strain S288c (Ab972)
C.Genetics:
A.Gene: MIPS:YDR371w
A.Map position: 4R
C.Superfamily: Serratia marcescens chitinase
C.Keywords: transmembrane protein
F:18-34/Domain: transmembrane #status predicted <TM>

```

[illegible]

C:Species: Streptomyces coelicolor
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 02-Jun-2000
C:Accession: T42074
R:Saito, A.; Fujii, T.; Yoneyama, T.; Redenbach, M.; Ohno, T.; Watanabe, T.; Miyashita, submitted to the EMBL Data Library, August 1998
A:Description: Structure of seven different chitinase genes from Streptomyces coelicolor
A:Reference number: 222056
A:Accession: T42074
A:Status: preliminary; translated from GB/EMBL/DDAJ
A:Molecule type: DNA
A:Residues: 1-417 <SAIT>
A:Cross-references: EMBL:AB017011; PIDN:BA075645.1
C:Genetics:
A:Gene: chid
C:Superfamily: Streptomyces chitinase chl40

Query Match 6.2%; Score 123.5; DB 2; Length 417;
Best Local Similarity 23.0%; Pred. No. 0.25;
Matches 64; Conservative 42; Mismatches 71; Indels 101; Gaps 16;

QY 55 IGGYPSWVSX--NNHNLKDLNPN-----LNVMHMSF-----AKMDSYDSI 93
DB 55 VGYFEMGVYDKNRYHKNHSSGSAKLTHTNPSGNTVGKCGAMGDVATATRAITAA 114
QY 94 ESTIVG-----SPLFKSLIGLEYIGLNEYFNAMNLRKARPDIMLSIGETV----- 142
DB 115 DSDVGVADPTWQD-----LRGNPNOLLKRLKQHPDLKILMSFGMTWSGGA 161
QY 143 ----HSSFS-DSALNVE--KIANLVDELFGDIDVDFE-PNGSFDGLN-DKEADDFVQ 193
DB 162 QAAQNEPAPQSCYDILVENSRRMDV-----FDGIDIDWEYFNAC--GLSCDTSGRDAFPK 214
QY 194 VYTKLREYMCDDKLISISOSNGALSCIGFNDPKIKCMDEAPYNSKYFNPDVKELLR 253
DB 215 LMGALNAKGGQDLYVTAATRADTAG-----GKI---DAADV----- 248
QY 254 AAOMASAGATYILMNNLKMIDMVFOTFNTYSTDST 291
DB 249 -----AGAAQY-----VDWYNPMTYDFPGAMDAT 272

RESULT 14
S56698
narbonin (clone pNag2) - *Vicia narbonensis*
N:Alternate names: 2S globulin
C:Species: *Vicia narbonensis*
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 05-Nov-1999
R:Accession: S56698; S56735; S44031
R:Nong, V.H.; Schlesier, B.; Bassuener, R.; Repik, A.; Horstmann, C.; Muentz, K.
Plant Mol. Biol. 28, 61-72, 1995
A:Title: Narbonin, a novel 2S protein from *Vicia narbonensis* L. seeds: cDNA, gene structure
A:Reference number: S56696; MUID:95306792
A:Accession: S56698
A:Molecule type: DNA
A:Residues: 1-291 <NONG>
A:Cross-references: EMBL:Z25533; NID:g9396824; PIDN:CAA80980.1; PID:g9396825
A:Accession: S56735
A:Molecule type: protein
A:Residues: 2-15;182-191,'E',193-195,'EE',198-207,250-251,'E',253-261,290-291 <NONG>
C:Superfamily: alcohol sulfotransferase
C:Keywords: seed; storage protein
E:2-291/Product: narbonin #status experimental <MANT>

Query Match 6.2%; Score 122; DB 2; Length 291;
Best Local Similarity 21.5%; Pred. No. 0.2;
Matches 72; Conservative 39; Mismatches 84; Indels 140; Gaps 18;

QY 72 LNPNLNVVMSFAKMDLSYDSIVGSPLL-FKSLIGLEYIGLNEYFN----- 120
DB 12 VKNSTTTLH-----DSPREIVNTETLEPHYILG---FAIESIYESGKGTGTFEES 58

QY 121 -----AMNLKRAPDILMLSLGGETYHPSFSDA-----LNAVEKIANLV--- 161
DB 59 MDVELFGPEKVKLRRBHEVKVVISIGRGVN-TPEDPAEENWVMSNAKESKLIIQYK 117
QY 162 -DEIG--FDGIDVYEPNGSPDGLNDEKADFFVQYTKLRKREIMCDKL-----ISISOS 214
DB 118 SDDSGNLIDGIDIHYEHRIS-----DEFPATLMGQLTTELK---DDDLINIVNSIAPSE 169
QY 215 NALSCIGFNDPKIKCMDEAPYNSKYFNPDVKELLRAAOMASAGATYILMNNLKMID 274
DB 170 N-----NSSHYK-----LYNAKKDYI 186
QY 275 DMVFVQTFNNTN--STDST--YVKELYSYAYYKRYDVIIMGF----- 315
DB 187 NMVDYQFSNOOKPYSTDADAVEIFEKSLKDY-----HPHKVLPGEFSTPLDTKHNKITYR 240
QY 316 -----TLMPSTPF-NPNCKMLYKSGD 337
DB 241 DIFIGCTRLVQTFSLPGVFEFMANDSVIPKRDGD 275

RESULT 15
S49898
hypoetical narbonin-like 2S protein (clone pYSNAG2) - spring vetch
C:Species: *Vicia sativa* (spring vetch, tare)
C:Date: 05-Mar-1995 #sequence_revision 14-Jul-1995 #text_change 23-Mar-2001
R:Accession: S49898
R:Nong, V.; Muentz, K.
submitted to the EMBL Data Library, November 1994
A:Description: A genomic sequence encoding putative narbonin from *Vicia sativa*.
A:Reference number: S49880
A:Accession: S49898
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-285 <NONG>
A:Cross-references: EMBL:Z46835; NID:g600112; PID:g600113
C:Superfamily: alcohol sulfotransferase

Query Match 6.1%; Score 121; DB 2; Length 285;
Best Local Similarity 21.1%; Pred. No. 0.23;
Matches 60; Conservative 55; Mismatches 89; Indels 80; Gaps 16;

QY 114 LNEYF--NDAMNLKRAPDILMLSLGGETYHPSFSDA-----LNAVEKIANLV----- 161
DB 59 MDEFPGDPKVKNNLKTKEHVKVVISIGRGVE--TPDPAPQNIWVSNVAKSLKLIQYK 117
QY 162 DEIG--FDGIDVYEPNGSPDGLNDEKADFFVQYTKL-REYMCDDKLISISOSNGAL 218
DB 118 NESGNLIDGIDINYEHRIS-----DEAFPRLLGQLITELKENDLNHVSTIAPSENNAS 172
QY 219 SCIGFNDPKIKCMDEAPYNSKYFNPDVKELLRAAOMASAGATYILMNNLKMIDMVF 278
DB 173 SYNL-----YNA-----NPPDI-----NLVDYGF 192
QY 279 VQTFNNTNSDS--YVKELYSYAYYKRYDVIIMGFYIMPPSPENPDNMLYKSG 336
DB 193 SNOLRHVSTEDADVDYKRVVNDY-----FTHKVLPGEFST-----DPLNMMYKITYR 239
QY 337 D-EYKTKNKKLRAD--GFGWMSLSDGNMAHNOQLAIEFVESL 377
DB 240 DIFIGCTRLKQTSPLPGVFEFMANDSNNG-DEPFKEVHLEEL 282

Search completed: May 8, 2002, 08:58:23
Job time: 76 sec


```

DR SMART; SM00495; ChIBD3; 1.
DR SMART; SM00060; FN3; 2.
DR PROSITE; PS01095; CHITINASE_18; 1.
KW Hydrolase; Glycosidase; Chitin degradation; signal; Repeat.
FT SIGNAL 1 41
FT CHAIN 42 699
FT DOMAIN 42 460 CHTINASE A1.
FT DOMAIN 465 549 CATALYTIC.
FT DOMAIN 560 644 FIBRONECTIN TYPE-III (R-1).
FT ACT_SITE 204 204 FIBRONECTIN TYPE-III (R-2).
FT ACT_SITE 200 200 PROTON DONOR (PROBABLE).
FT MUTAGEN 200 200 D->N: DECREASE IN ACTIVITY.
FT MUTAGEN 200 200 D->E: NO CHANGE IN ACTIVITY.
FT MUTAGEN 204 204 E->D,Q: LOSS OF ACTIVITY.
SQ SEQUENCE 699 AA; 73677 MW; AC7C9B22E2987643 CRC64;

Query Match 8.6%; Score 169.5; DB 1; Length 699;
Best Local Similarity 20.0%; Pred. No. 0.00021;
Matches 88; Conservative 58; Mismatches 113; Indels 181; Gaps 21;

OY 55 IGGYPSWVSY--NHNLDKLNPNLVHMSFAKMDLSYDSIES----- 95
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 46 IGVGYPSMAVAGRYNVNADIDPT-KVHINAYAFADICWNGHGNPDSPGPNVYTCQNE 104
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 96 -----IVGSPLEFKSLGLEXYIG-----LNEYFDAMNLRKARPDITMLSL 137
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 105 KSOTINPNGTIVIGDEPWID---TGKTFAGDTWDPPIAGININQLKTKOTNPNLKTITISV 161
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 138 GGEYHSPSPSALNAV--EKIAN-LVDEL---GFDGIDVYVE--PNSFPGLNKKEKAD 189
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 162 GGMWMSRFSVVAATPAREFANSADFLKRYNDGVLMEYFVSGGLDQ--NSKRPE 220
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 190 --FVQVYVTKLREYMCDDKLISISOSNGALSCIGFNPCKKICMDEAPNYSKYENKPDV 247
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 221 KQNTLLSKREL-----DAAGAV-----DG 243
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 248 KKEILRAQMASAGCAIYLMN---NLKMDIMVFOVTNTNSTDSTVMKEL---YYSY 300
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 244 KKYLL---TASGASATYAAANTELAIAIVDWINIMTYDNGAMQKISAHNAPLNYDPA 300
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 301 A-----YYSKKYD----- 308
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 301 ASAAGVDANTFNVAAGQHLNAGVPAKLVLGVPYGRKMDGCAQAGNGOYOTCTGGS 360
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 309 -----YVIMGFILMFSTP-----FNPNDKMLV-----KSIDGVK 340
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 361 SVGTWEGSFDFYDLNAYINKNGYTRYMNDTAKVPIYLNASKRFISYDAESVG--YK 418
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 341 TENKLNKRADFGGLMSLSD 360
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 419 TAYIKSKGLGCGAMEWELSGD 438
| | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 2
CHIT_STRPL STANDARD; PRT; 610 AA.
ID CHIT_STRPL
AC P11220;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DR 01-FEB-1995 (Rel. 31, Last annotation update)
DE CHITINASE 63 PRECURSOR (EC 3.2.1.14).
GN CHTA.
OS Streptomyces plicatus.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomyocineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID:1922;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-92192480; PubMed-1532161;
RA Robbins P.W., Albright C., Benfield B., Pero J.;
RT "Cloning and high-level expression of chitinase-encoding gene of
RT Streptomyces plicatus.";
RL Gene 11:69-76(1992).

```

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RN [2]
RP SEQUENCE OF 1-45 FROM N.A., AND SEQUENCE OF 31-45.
RX MEDLINE-88087127; PubMed-3275646;
RA Robbins P.W., Albright C., Benfield B.;
RT "Cloning and expression of a Streptomyces plicatus chitinase
RT (chitinase-63) in Escherichia coli.";
RL J. Biol. Chem. 263:443-447(1988).
CC -1 CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF
CC -1 ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
CC -1 INDUCTION: BY CHITIN.
CC -1 SIMILARITY: BELONGS TO CHITINASE CLASS II (FAMILY 18 OF GLYCOSYL
CC -1 HYDROLASES).
CC -1 SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC -1 SIMILARITY: CONTAINS 1 BACTERIAL-TYPE CELLULOSE-BINDING DOMAIN
CC (CBD).
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M82804; AAA26720.1; .
DR EMBL; M18397; AAA26717.1; -.
DR PIR; A29912; A29912.
DR PIR; JH0573; JH0573.
DR HSSP; P07986; 1EXH.
DR InterPro; IPR001919; CBD_2.
DR InterPro; IPR001579; Chitinase_2.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR001777; FN_III.
DR InterPro; IPR001223; Glyco_hydro_18.
DR Pfam; PF00553; CBD_2; 1.
DR Pfam; PF00041; fn3; 1.
DR Pfam; PF00704; Glyco_hydro_18; 1.
DR SMART; SM00060; FN3; 1.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
DR PROSITE; PS00561; CBD_BACTERIAL; 1.
DR PROSITE; PS01095; CHITINASE_18; 1.
KW Hydrolase; Glycosidase; Chitin degradation; Chitin-binding; signal.
FT SIGNAL 1 30
FT CHAIN 31 610
FT DOMAIN 35 140 CHTINASE 63.
FT DOMAIN 148 229 CELLULOSE-BINDING.
FT DOMAIN 236 610 FIBRONECTIN TYPE-III.
FT ACT_SITE 383 383 CATALYTIC.
FT ACT_SITE 383 383 PROTON DONOR (BY SIMILARITY).
FT CONFLICT 3 3 F->I (IN REF. 2).
SQ SEQUENCE 610 AA; 63974 MW; 6A202EF361CDD500 CRC64;

Query Match 7.1%; Score 140.5; DB 1; Length 610;
Best Local Similarity 21.4%; Pred. No. 0.017;
Matches 79; Conservative 51; Mismatches 108; Indels 131; Gaps 17;

OY 34 GESKNPREIITKTFESGKGIIGYPSWVSY--NHNLDKLD-----NPNLN----- 77
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 232 GEPNPNP-----GAEYKMGYFTNWGYYGNVHVKNLNYSGSAEKTHINLRFNGV 281
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 78 -----VHMSFAKMDLSYDSIESIVG-----SPLFKSLGLEXYIGLNEYFDAMNLRK 126
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 282 QGKCTTGDAVADYKRAVDADSVGDVADTWDP-----LRANFQNLRLKA 328
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 127 ARPDITMLISIGETY-----HSSPDSALNAVETKANLVDELGFGIDVYE--PN 176
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 329 EYPIKILYSGFTWGGGPDPAVKNPAAKSCHDVDEPRNADV--FDGIDLWDEYRN 366
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 177 GSFGLDKREKADPEFYVTKLREYMCDDKLISISOSNGALSCIGFNPCKKICMDEAP 236
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 387 ACGISCDETSAPNAPFSSMKAMRAEFGQDYLITTAAYVADG-----SDGKIL---DAAD 436
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 237 YN--SKYFNKPDVKKELLRAQMASAGCAIYLMNLDKMDIMVFOVTNTNSTDSTVMK 294
| | | | | | | | | | | | | | | | | | | | | | | | | | | |

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Db 437 YGASKY-----IMWYNTYDF-----454

Qy 295 ELYDSYAYG-----KKDYVIMGFTLMFPSTPPN---PNDKMLVKSIGDFVTE 342

Db 455 --FGMAKNGPAPSPPLNADGIRQOGFTTADAMAKRKSQVPRADKILI-GIGYGGW 511

Qy 343 NKLNRKADG 351

Db 512 TGVTSAPG 520

RESULT 3

CHIT1_COCIM STANDARD; PRT; 427 AA.

AC P54196;

DT 01-FEB-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 01-OCT-1996 (Rel. 34, Last annotation update)

DE ENDOCHITINASE 1 PRECURSOR (EC 3.2.1.14) (COMPLEMENT-FIXATION ANTIGEN) (CF-ANTIGEN) (CF-Ag).

GN CTS1.

OS Coccidioides immitis.

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;

OC Onygenales; mitosporic Onygenales; Coccidioides.

OX NCBI_TaxID=5501;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C735;

RX MEDLINE=96144270; PubMed=8566773;

RA Pishko E.J., Kirkland T.N., Cole G.T.;

RT "Isolation and characterization of two chitinase-encoding genes (cts1, cts2) from the fungus Coccidioides immitis."

RL Gene 167:173-177(1995).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=SLIVEIRA;

RA Yang C., Zhu Y., Magee D.M., Cox R.A.;

RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.

CC -1- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.

CC -1- SIMILARITY: BELONGS TO CHITINASE CLASS II (FAMILY 18 OF GLYCOSYL HYDROLASES).

CC -----

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CC -----

CC EMBL: LA1663; AAA92643.1; -

DR EMBL: U51271; AAA96515.1; -

DR EMBL: U33265; AAB06687.1; -

DR HSP: P07254; ICTN.

DR InterPro: IPR001579; Chitinase_2.

DR InterPro: IPR001223; Glyco_hydro_18.

DR Pfam: PF00704; Glyco_hydro_18; 1.

DR PROSITE: PS01095; CHITINASE_18; 1.

KW Hydroxylase; Glycosidase; Chitin degradation; Chitin-binding; Signal;

KW Glycoprotein.

FT SIGNAL 1 ?

FT CHAIN 1 ?

FT CARBOHYD 387 427

FT CONFLICT 15 47

FT CONFLICT 199 199

FT SEQUENCE 427 AA; 47629 MW; 1C396DBDB1A7001A CRC64;

Query Match 6.7%; Score 132.5; DB 1; Length 427;

Best Local Similarity 25.3%; Pred. No. 0.039;

Matches 62; Conservative 39; Mismatches 65; Indels 79; Gaps 12;

Qy 124 LKRAPDIIMLSIGETYYHSPDSALNAVE---KIAN---LYDELGFDGIDVYE-P 175

Db 115 LKNNRNKLTLLSIGWYSP-NFKTPASTEGRKKFPDLSLKKDLGFDGIDVYE-P 173

Qy 176 NSGFDGLNDEKADFFVOYVTKLRMCDDKLTISQSSNGALSCIGFNDPKICMDDEA 235

Db 174 -----EDEKQANDFVLL-----KACREALD 194

Qy 236 PYSKATFNKPYKKELELRAQMASAGAIYLMNNLKD---IDWVFQTFNTNSTD--S 290

Db 195 AYSAKH---PNSKFLTLTA--SPAGPQYKTKLAEMDKYIDFNNLMAIDFGSGMDVYS 249

Qy 291 TYMKELYDSYAYGKKDYVIMGFTLMFPSTPPNNDKMLVKSIGDFVTEKLNKRAD 350

Db 250 GMSNVFPS-----TTKPESTPFSSD-----KAVKDYIKAGVPANKIVL 288

Qy 351 GFGMW 355

Db 289 GMPLY 293

RESULT 4

CHIT4_TRIHA STANDARD; PRT; 423 AA.

AC P48827;

DT 01-FEB-1996 (Rel. 33, Created)

DT 01-FEB-1996 (Rel. 33, Last sequence update)

DT 15-DEC-1998 (Rel. 37, Last annotation update)

DE 42 KDA ENDOCHITINASE PRECURSOR (EC 3.2.1.14).

GN CHIT42.

OS Trichoderma harzianum.

OC Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Trichoderma.

OX NCBI_TaxID=5544;

RN [1]

RP SEQUENCE FROM N.A., AND SEQUENCE OF 35-52; 93-107; 371-385 & 397-414.

RX MEDLINE=95269313; PubMed=7750151;

RA Garcia I., Lora J.M., de la Cruz J., Benitez T., Llobell A.,

RA Plator-Toro J.A.;

RT "Cloning and characterization of a chitinase (chit42) cDNA from the mycoparasitic fungus Trichoderma harzianum."

RL Curr Genet. 27:83-89(1994).

CC -1- FUNCTION: MORPHOGENETIC ROLE DURING APICAL GROWTH, CELL DIVISION AND DIFFERENTIATION (CELL WALL MORPHOGENESIS). ANTIFUNGAL AGENT.

CC -1- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.

CC -1- SUBCELLULAR LOCATION: SECRETED. BY CHITIN AND IS CARBOHYLITE REPRODUCED.

CC -1- INDUCTION: SPECIFICALLY INDUCED BY CHITIN AND IS CARBOHYLITE REPRODUCED.

CC -1- SIMILARITY: BELONGS TO CHITINASE CLASS II (FAMILY 18 OF GLYCOSYL HYDROLASES).

CC -----

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CC -----

CC EMBL: S78423; AAB34355.1; -

DR HSP: P07254; ICTN.

DR InterPro: IPR001579; Chitinase_2.

DR InterPro: IPR001223; Glyco_hydro_18.

DR Pfam: PF00704; Glyco_hydro_18; 1.

DR PROSITE: PS01095; CHITINASE_18; 1.

KW Hydroxylase; Glycosidase; Chitin degradation; Signal; Zymogen;

KW Chitin-binding.

FT SIGNAL 1 22

FT PROPEP 23 34

FT CHAIN 35 423

42 KDA ENDOCHITINASE.

FT ACT_SITE 171 171 PROTON DONOR (BY SIMILARITY).
 FT CARBOHYD 218 218 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 423 AA; 46056 MW; DF90378BED1C30BE CRC64;

Query Match 6.6%; Score 130.5; DB 1; Length 423;
 Best Local Similarity 21.6%; Pred. No. 0.053;
 Matches 83; Conservative 56; Mismatches 131; Indels 115; Gaps 19;

QY 8 SFL-VICLCLSTVSVYEGHRRARGESRKNPREIKTFKESGKIIOG-YIPSNVS 64
 DB 3 SFLGKSVALLAALQATLSSPKRGHRRASVEKRN-----GYANSVFTMGIGI 49
 QY 65 YNNHLK--DLNPNLVNVMHSEKMDLSYDSIESIYGSPLFKSLGLEIY-----IG 113
 DB 50 YDRNFQADLVAS-DYVHVHVSFPMLOAD-----GTVISDPTADYKHKHADSMDNVG 102
 QY 114 LNEY--FNDAMNLRKAPDITMLISLGGETVHPSSFDAL-----NAVERIANLVDEL 164
 DB 103 TNAVGCYKQLFYKVKANRGLKVLISIGGWTW-STNFPASASTDANRKNFAKTATFEMKDW 161
 QY 165 GFGIDVDYEPNGSFDLNDKERADFEYQVYTKLREYWCDDKLISISSNGALSCIGFN 224
 DB 162 GFGIDIDW-----ETPAD-----ATQASNNILLL----- 186
 QY 225 DPKRICMDDEAPYNSKYFNKPKYKELLRAAQAASAGAIYLMNNLKMDIMVEVQETNY 284
 DB 187 --KEVRSQORDA-YAAQY--APGYHFLITLAPACKDNYSKRLADLGQVLYINLMAYDY 241
 QY 285 TNSIDTSVME--LYDSIAYIKKRYDVIYIMGFILMPS-----IPFNDKMKLVKSIDF 338
 DB 242 AGSFSPITGHDANLENN-----PSNDAATPFMTD-----SAVDY 276
 QY 339 VKTENKLNKRADFGELSLSSDNA 363
 DB 277 INGVPRANKIVLGMPIYGRSPQNTA 301

RESULT 5
 CHIA_SERMA STANDARD; PRT; 563 AA.
 ID CHIA_SERMA STANDARD; PRT; 563 AA.
 AC P07254; O54275.
 DT 01-APR-1988 (Rel. 07, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE CHITINASE A PRECURSOR (EC 3.2.1.14).
 GN CHIA.
 OS Serratia marcescens.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Serratia.
 NCBI_TaxID=615;
 RX SEQUENCE FROM N.A.
 RA Koo J.C., Lim C.O., Choi Y.J., Kim C.Y., Bank J.D., Lee S.Y.,
 RA Cho M.J.;
 RA Submitted (JAN-1993) to the EMBL/GenBank/DBJ databases.
 RP SEQUENCE FROM N.A.
 RC STRAIN-ATCC 990 / OMB1466;
 RA Jones J.D.G., Grady K.L., Suslow T.V., Bedbrook J.R.;
 RT "Isolation and characterization of genes encoding two chitinase
 RT enzymes from Serratia marcescens.";
 RL EMBO J. 5:467-473(1986).
 RN [3]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 24-31.
 RC STRAIN-BJ1200.
 RA MEDLINE=95154677; PubMed=7851747;
 RA Bruberg M.B., Eljink V.G.H., Nes I.F.;
 RT "Characterization of a chitinase gene (chia) from Serratia marcescens
 RT BJ1200 and one-step purification of the gene product.";
 RL FEMS Microbiol. Lett. 124:399-404(1994).
 RN [4]
 REVISONS, AND X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).

RX MEDLINE=95219379; PubMed=7704527;
 RA Perrakis A., Tews I., Dauter Z., Oppenheim A.B., Chet I., Wilson K.S.,
 RA Vorgias C.E.;
 RT "Crystal structure of a bacterial chitinase at 2.3-A resolution.";
 RL Structure 2:1169-1180(1994).
 CC -1- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF
 CC N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
 CC -1- SIMILARITY: BELONGS TO CHITINASE CLASS II (FAMILY 18 OF GLYCOSYL
 CC HYDROLASES).
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; L01455; AAA26551.1; -;
 DR EMBL; X03657; CAA27292.1; -;
 DR EMBL; Z36294; CAA85291.1; -;
 DR PIR; A25090; A25090.
 DR PDB; 1CTN; 20-JUL-95.
 DR InterPro; IPR001579; Chitinase_2.
 DR InterPro; IPR001223; Glyco_hydro_18.
 DR InterPro; IPR000601; PKD_domain.
 DR Pfam; PF00704; Glyco_hydro_18; 1.
 DR SMART; SM00089; PKD; 1.
 DR PROSITE; PS01095; CHITINASE_18; 1.
 KW Hydrolyase; Glycosidase; Chitin degradation; Signal; 3D-structure.
 FT SIGNAL 1 23
 FT CHAIN 24 563
 FT DOMAIN 150 563
 FT ACT_SITE 315 315
 FT ACT_SITE 391 391
 FT CONFLICT 52 52
 FT CONFLICT 73 73
 FT CONFLICT 76 77
 FT CONFLICT 79 79
 FT CONFLICT 121 121
 FT CONFLICT 139 139
 FT CONFLICT 226 226
 FT CONFLICT 395 395
 FT CONFLICT 410 430
 FT CONFLICT 437 437
 FT CONFLICT 464 467
 FT CONFLICT 473 473
 FT CONFLICT 484 484
 SQ SEQUENCE 563 AA; 60979 MW; 0696FE6AF83AA35 CRC64;

Query Match 6.5%; Score 128.5; DB 1; Length 563;
 Best Local Similarity 20.7%; Pred. No. 0.11;
 Matches 97; Conservative 63; Mismatches 179; Indels 129; Gaps 24;

QY 2 NFTV-----KYSFLVYICLC-----CLSTYVSVI-----EGHRRARGESRKNP-REIKTFK 48
 DB 99 NFKXNKGGRYQMOY--ALCNADGCTASDAIEIYVADIDGSHLP---LKEPFLKKNPKYK 153
 QY 49 ESGGIIIGYPPSVSNHNLK-DLNPNVNVMHSEKMDLS-----YDSIESVGS-PL 101
 DB 154 QNSGKVVGSYFVEGWYGRNFTVDKIPAQNIPLHLYGFIPICGNGINSLKKEISGFOA 213
 QY 102 LFKSLIGLEIYGLNEY-----FNDAMNLRKAPDITMLISG 138
 DB 214 LQRCQGRDEPKXSIHDPFALQAKQGYTAMDPKYKNGGQIMALKQAHPDILKIPSG 273
 QY 139 GETYHPSSF-----DSALNAVERKIANLVDELFGIDVDVE---PNSGFGINDKER 187
 DB 274 GWTISDPEFFFMGDKVKKDRYGVSKFE--LQTKMFEFGVLDIDEPFGGKCANPNLSPD 331
 QY 188 ADFEVQVYTKLREYMCDD-----KLISISSNGALSCIGFNDPKK-----ICM 231

DB 320 VIAGAGSSVYTKOTYGRYELLIFRANFTPSHAQTIGFTTOLSDNDGVGWMYDWTGNPPE 379

OY 328 DKMLV-----KSIGDFYKTEK-LNKRADGFLMSLSDNA-----HNEOLATEY 372

DB 380 LTRWVSGSDIDGDPVNSNKYLK-----FYIDLKRISTDTLNFITFDLTIDLEY 431

RESULT 11

DRTS_PLABA STANDARD; PRT; 587 AA.

AC 027713; 027714; (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DE BIFUNCTIONAL DIHYDROFOLATE REDUCTASE-THYMIDYLATE SYNTHASE (DHFR-TS) [INCLUDES: DIHYDROFOLATE REDUCTASE (EC 1.5.1.3); THYMIDYLATE SYNTHASE (EC 2.1.1.45)].

OS Plasmodium berghei (strain Anka).

OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

OX NCBI_TaxId=5823;

RP SEQUENCE FROM N.A.

RA MEDLINE=95198769; PubMed=7891743;

RT van Dijk M.R., McConkey G.A., Vinkenoog R., Waters A.P., Janse C.J.;

RT "Mechanisms of pyrimethamine resistance in two different strains of Plasmodium berghei."

RL Mol. Biochem. Parasitol. 68:167-171(1994).

CC [2]

RP SEQUENCE OF 12-201 FROM N.A.

RA MEDLINE=95059225; PubMed=7969277;

RT Cheng Q., Saul A.;

RT "The dihydrofolate reductase domain of rodent malarial: point mutations and pyrimethamine resistance."

RL Mol. Biochem. Parasitol. 65:361-363(1994).

CC -1- CATALYTIC ACTIVITY: 5,6,7,8-TETRAHYDROFOLATE + NADP(+) = 7,8-DIHYDROFOLATE + NADPH.

CC -1- CATALYTIC ACTIVITY: 5,10-METHYLENETHETRAHYDROFOLATE + DUMP = DIHYDROFOLATE + DUMP.

CC -1- PATHWAY: ESSENTIAL STEP FOR DE NOVO GLYCINE AND PURINE SYNTHESIS, DNA PRECURSOR SYNTHESIS, AND FOR THE CONVERSION OF DUMP TO DIMP.

CC -1- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE DIHYDROFOLATE REDUCTASE FAMILY.

CC -1- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE THYMIDYLATE SYNTHASE FAMILY.

CC -----

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CC -----

DR EMBL: U12275; AAB60237.1; -

DR EMBL: L28119; AAA29581.1; -

DR HSSP: P00470; IAN5.

DR InterPro: IPR001796; DHFR.

DR InterPro: IPR000398; Thymidylat_synth.

DR Pfam: PF00186; Dihfolate_red; 1.

DR Pfam: PF00303; thymidylat_synth; 1.

DR PRINTS: PR00070; DHFR.

DR PRINTS: PR00108; THYMSDNTHASE.

DR PRODOM: PD001180; Thymidylat_synth; 1.

DR PROSITE: PS00091; DHFR; 1.

DR PROSITE: PS00091; THYMIDYLATE_SYNTHASE; 1.

KW Multifunctional enzyme; Oxidoreductase; Transferase; NADP; Nucleotide biosynthesis; One-carbon metabolism.

KW Methyltransferase; Nucleotide biosynthesis; One-carbon metabolism.

FT DOMAIN 1 240 DIHYDROFOLATE REDUCTASE.

FT ACT_SITE 301 587 THYMIDYLATE SYNTHASE.

FT VARIANT 110 469 BY SIMILARITY.

FT VARIANT 110 469 S -> N (IN PYRIMETHAMINE RESISTANCE).

FT VARIANT 177 177 S -> F (IN PYRIMETHAMINE RESISTANCE).

SQ SEQUENCE 587 AA; 68932 MW; 6E638C2B02EFC13A CRC64;

Query Match 5.4%; Score 108; DB 1; Length 587;

Best Local Similarity 18.7%; Pred. No. 2.9;

Matches 80; Conservative 67; Mismatches 132; Indels 148; Gaps 20;

OY 7 YSFLVICLLCCLSTVYVIEGHRAPGESRKNPRELIKTFKESGK-----IIGG 57

DB 8 FDIYAICACCKVLN-----DDEKVRCEFN-----KTFKIGIAGVLPWMCNLIIDMK 53

OY 58 YPESWVSY-----NHNK-----DLNPNL-----NVVNH-----SEPAK 85

DB 54 YFSSVTYIENNNYIRLWKRDYKMEKHNKNVNEIPLTNIISSTNNLQNTVWKKRWS 113

OY 86 MDLSYDSIESIVGSPILFKSLIGLEYGLNEFDANLKRAPDIIMLS----- 136

DB 114 IPKFKELQNRILNIIISRLKKEDIVNENNNNNNIIITSVDLFPILKCKYKCP 172

OY 137 LGGETYHPSSFDALNAVERIANLVDLGFIDVDYEPNGSFDGLNDEKADFPVQVYT 196

DB 173 IGSSTVYKPELD-----RNLIKRIYPTIRINSYNCVLPPEINE-----NLF----- 214

OY 197 KLRPYMDDKLISTQ-----SSNGALSCIGFNDKRCICMDEAPYNS----- 239

DB 215 -----KITSIDVYNSNNTLDFIYSKTEINPEVNNPFLGVCDQKAPFD 265

OY 240 ----KYF-----NKPDVKELLRAQMASAGATYLMNNLMDIMVFOVFTNSTDST 291

DB 266 EDDVTYFSFNKKNKNIKNSHA-----HNEK-----IYNSIKKKNHPEQ 306

OY 292 VMKELDYSAVYGGKYDYVII-----MGFTLMPSPDPNP-----NDKMLYKSID-----FV 339

DB 307 YLNIIVYIIMGNKQDDRTGVGLSKFGYMKMKNLNEYPLLTTRKILFIRGILIELLWPI 366

OY 340 KTEKN 346

DB 367 RGETNGN 373

RESULT 12

CHIT_MANSE STANDARD; PRT; 554 AA.

ID CHIT_MANSE

AC P36362;

DT 01-JUN-1994 (Rel. 29, Created)

DT 01-JUN-1994 (Rel. 29, Last sequence update)

DT 01-FEB-1995 (Rel. 31, Last annotation update)

DE ENDOCHITINASE PRECURSOR (EC 3.2.1.14).

OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;

OC Sphingidae; Sphingidae; Sphinginae; Manduca.

OX NCBI_TaxId=7130;

RN [1]

RP SEQUENCE FROM N.A.

RA MEDLINE=93357793; PubMed=8353525;

RT Kramer K.J., Corpuz L., Choi H.K., Muthukrishnan S.;

RT "Sequence of a cDNA and expression of the gene encoding epidermal and gut chitinases of Manduca sexta."

RL Insect Biochem. Mol. Biol. 23:691-701(1993).

RN [2]

RP SEQUENCE FROM N.A.

RA MEDLINE=97215580; PubMed=9061927;

RT Choi H.K., Choi H.K., Kramer K.J., Muthukrishnan S.;

RT "Isolation and characterization of a genomic clone for the gene of an insect molting enzyme, chitinase."

RL Insect Biochem. Mol. Biol. 27:3-47(1997).

CC -1- FUNCTION: DIGEST CHITIN IN THE EXOSKELETON DURING THE MOLTING PROCESS.

CC -1- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.

CC -1- SUBCELLULAR LOCATION: SECRETED.

CC -1- TISSUE SPECIFICITY: EPIDERMIS AND GUT.

CC -1- DEVELOPMENTAL STAGE: HIGH LEVELS SEEN IN THE EPIDERMIS ON DAY 0,
CC BUT RAPIDLY DISAPPEARS AND IS UNDETECTED ON DAYS 1-4 OF FIFTH
CC INSTAR. IT REAPPEARS ON DAY 5 AND PEAKS ON DAY 7 AFTER WHICH A
CC RAPID DECLINE IS SEEN. IN THE CUT IS DETECTED ON DAY 6 WITH LOWER
CC LEVELS SEEN ON DAYS 0, 7 AND 8.
CC -1- SIMILARITY: BELONGS TO CHITINASE CLASS II (FAMILY 18 OF GLYCOSYL
CC HYDROLASES).
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U02270; AAC04924.1; -
CC EMBL: L49234; AAB53952.1; -
CC InterPro: IPR002557; Chitin_binding.
CC InterPro: IPR001579; Chitinase_2.
CC InterPro: IPR001223; Glyco_hydro_18.
CC Pfam: PF01607; Chitin_bind_2; 1.
CC Pfam: PF00704; Glyco_hydro_18; 1.
CC SMART: SM00494; CHBD2; 1.
CC PROSITE: PS01095; CHITINASE_18; 1.
CC HydroLase: glycosidase; Chitin degradation; signal; glycoprotein.
CC FT SIGNAL 1 19 POTENTIAL.
CC FT CHAIN 20 554 ENDOCHITINASE.
CC FT DOMAIN 396 453 SER/THR-RICH.
CC FT ACT_SITE 146 146 PROTON DONOR (BY SIMILARITY).
CC FT CARBOHYD 85 85 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 303 303 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 407 407 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 545 545 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT SEQUENCE 554 AA; 62203 MW; 3989D756C9CD490 CRC64;
SO
Query Match 5.4%; Score 107; DB 1; Length 554;
Best Local Similarity 20.4%; Pred. No. 3.1;
Matches 32; Conservative 40; Mismatches 57; Indels 28; Gaps 6;
OY YPSWVSY-----NHNKLDNPNLVNVMSPAKMDLYDSIESVIGSLPKSLGLEIYI 112
DB 28 YFSNMAVYRPVGKRGYIDT-PVEKCHITITYSFIVTEGENSEVLIDDELVDKNG----- 82
OY 113 GLNEFYNDAMNLRKAPDIIIMLSIGETYPSPS-----DSALNAVEKIANLVDELG 165
DB 83 -----FRNFTSLRBSHPVKRMVAVGVMAEGSSKSHVNAQSTMTSIRSVSILKXYD 137
OY 166 FDGIDVDYEPNGSFD--GLNDKEKADFFVOYVTKLR 199
DB 138 FDGLDLMVEYPGADRGSGFSDDKDK---FLYVQELR 171
RESULT 13
YK04_YEAST STANDARD; PRT; 758 AA.
ID YK04_YEAST
AC P36096;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE HYPOHETICAL 87.9 KDA PROTEIN IN PTM-1RX1 INTERGENIC REGION PRECURSOR.
GN YK1034W OR YK1247.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_Taxid=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RX MEDLINE=94262309; PubMed=8203146;
RA Purnelle B., Skala J., van Dyck L., Goffeau A.;
RT "Analysis of an 11.7 kb DNA fragment of chromosome XI reveals a new

RT tRNA gene and four new open reading frames including a leucine zipper
RT protein and a homologous to the yeast mitochondrial regulator ABF2.";
RL Yeast 10:125-130(1994).
RN [2]
RP SEQUENCE OF 1-570 FROM N.A.
RC STRAIN=S288C;
RX MEDLINE=93127731; PubMed=1481573;
RA Purnelle B., Skala J., van Dyck L., Goffeau A.;
RT "The sequence of a 12 kb fragment on the left arm of yeast chromosome
RT XI reveals five new open reading frames, including a zinc finger
RT protein and a homolog of the UDP-glucose pyrophosphorylase from
RT potato.";
RL Yeast 8:977-986(1992).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC -----
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CC -----
CC EMBL: X71622; -: NOT_ANNOTATED_CDS.
CC EMBL: X69584; CAA49298.1; -
CC EMBL: Z28034; CAA81869.1; -
CC PIR: S37855; S37855.
CC SGD: S0001517; YK1034W.
CC InterPro: IPR001841; Znf_ring.
CC Pfam: PF00097; Zf-C3HC4; 1.
CC SMART: SM00184; RING; 1.
CC Hypothetical protein: Transmembrane; Signal.
CC FT SIGNAL 1 26 POTENTIAL.
CC FT CHAIN 27 758 HYPOHETICAL PROTEIN YK1034W.
CC FT TRANSMEM 400 456 POTENTIAL.
CC FT TRANSMEM 440 456 POTENTIAL.
CC FT TRANSMEM 461 477 POTENTIAL.
CC FT TRANSMEM 528 544 POTENTIAL.
CC FT TRANSMEM 607 623 POTENTIAL.
CC FT TRANSMEM 638 654 POTENTIAL.
CC FT SEQUENCE 758 AA; 87879 MW; F29A61E994F96628 CRC64;
SO
Query Match 5.4%; Score 107; DB 1; Length 758;
Best Local Similarity 20.0%; Pred. No. 4.7;
Matches 61; Conservative 50; Mismatches 92; Indels 102; Gaps 14;
OY 62 WSYVHNKLDNPNLVNVMSPAKMDL---SYDSIESVIGSLPKSLGLEIYGLMEY 117
DB 114 WNTSNDASNLFPN-NINSTLGLKIDLVSNKKYKIR-----MPVPRF 155
OY 118 FNDAMNLRKAPDIIIMLSIGETYPSPS-----HPSPDSALNAVE--KIANLVDELG 165
DB 156 YEPATDFSEDIPP-----EGETYSWSPSYGELHANSFQHGELAIQISHSNQLQDNNN 208
OY 166 FDGIDVDYEPNGSFDGLN-----DKERADFFVOYVTKLREYMKDDKLISQSSNG 216
DB 209 YLRNFIKKNDKRWKLLNLQIDFSDKAKEKHSIYSKAVYDIOR---GRILSIQSSK- 263
OY 217 ALSCIGFND---FKKIDMDEAPYNSKYFKNKPDYKKELLRAAQASAGAIYLMNNIKD 272
DB 264 -----FISLFPALPHYMSFOND--YNEKIF-----NDVKE 290
OY 273 MIDWVFVTFNVTNSTDSTVKKELYSAYYAGKKRYVYIINGFTLMPSPFPNPKMLY 332
DB 291 LVD---EFMFTDTTDMTKVDVADYNNANFKCEYLIFLQL-----EFMNTYTRDOT 340
OY 333 KSIGD 337
DB 341 KLIDD 345
RESULT 14

```

POL1_SCHPO
ID PD11_SCHPO STANDARD; PRT: 492 AA.
AC Q10057;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE PUTATIVE PROTEIN DISULFIDE ISOMERASE C1P5.02 PRECURSOR (EC 5.3.4.1).
GN SPAC1P5.02.
OS Schizosaccharomyces pombe (fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomyces.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RA Gentles S., Odell C., Churcher C.M., Barrell B.G., Rajandream M.A.,
RA Walsh S.V.;
RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PARTICIPATES IN THE FOLDING OF PROTEINS CONTAINING
CC DISULFIDE BONDS, MAY BE INVOLVED IN GLYCOSYLATION, PROYL
CC HYDROXYLATION AND TRIGLYCERIDE TRANSFER (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: REARRANGEMENT OF BOTH INTRACHAIN & INTERCHAIN
CC DISULFIDE BONDS IN PROTEINS TO FORM THE NATIVE STRUCTURES.
CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN (BY SIMILARITY).
CC -1- SIMILARITY: CONTAINS 2 THIOREDOXIN DOMAINS.
CC -----
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CC -----
DR EMBL: Z68136; CAA92230.1; -.
DR HSSP: P07237; IMEX.
DR InterPro: IPR000886; ER_target.
DR InterPro: IPR000063; ThioRed.
DR Pfam: PF00085; ThioRed. 2.
DR PRINTS: PRO0421; THIOREDOXIN.
DR PROSITE: PS00014; ER_TARGET; 1.
DR PROSITE: PS00194; THIOREDOXIN; 2.
KW Hypothetical protein; Redox-active center; Isomerase;
KW Endoplasmic reticulum; Repeat; Signal.
FT CHAIN 1 22 POTENTIAL.
FT SIGNAL 23 492 PUTATIVE PROTEIN DISULFIDE ISOMERASE
FT C1P5.02.
FT DISULFID 51 54 REDOX-ACTIVE (BY SIMILARITY).
FT FT 385 388 REDOX-ACTIVE (BY SIMILARITY).
FT CARBOHYD 161 161 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 257 257 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT SITE 489 492 PREVENT SECRETION FROM ER (POTENTIAL).
SQ SEQUENCE 492 AA; 54880 MW; C50B59236566667 CRC64;

Query Match 5.3%; Score 105; DB 1; Length 492;
Best Local Similarity 20.9%; Pred. No. 3.7;
Matches 93; Conservative 59; Mismatches 162; Indels 132; Gaps 19;

18 LSTVYVIGHARAPESRRKPREIKTFESGKGIIGYPPSVASNNHKLQDNP--- 74
11 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
6 LLAALFALFSGGFCASAEVKKVKEGLNELITAKVLAKVTAWCGH---CKALAPYE 62
11 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
75 ---NNVVMSPAKMDLSDY---SIESIVGSPL--FKSLIGL-EXYIGLNEYENDAMN 123
11 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
63 SADELKEDISLVEVCTEGDLCSEYSIRGYPTLVNFKNGKQISQSGPKRH--DAL- 119
11 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
124 LKARADITMLLSGGTTPSPSFDALNAVEKIANLVDELGFGIDVDYPPNSFDGLN 183
11 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
120 VKYMRQLD-----PTVAPISKDTLENVEK---ADLAVALVAFFKDKLNDTY---- 164
11 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
184 DKRAKDAFFVQYVTKLRREYMDOKLISISQSSNGALSCIGFNDPKICMDDEAPYNSKRYN 243
11 : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

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Db 165 -----TEVAEVMKDDVEVFAASDDKEKLAKS--LGSNFPQIVAFYTKDAADS----- 207
11 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 244 KPDYKELLRAAOMASAGAIYIMNNLKDMDVWFVOTFN-----YTNSTDP 291
11 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 208 -----DKLVYGDWDMPASIADFIGVSSIPLLDELNMTFGYQSGPLGIIFYNSTES- 261
11 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 292 VKMELYDSYANYGKKYDYVITMGF-----TLMPST 322
11 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 262 -RDELYDVFQPLARKYODTLRF AFLDAVRGAVAKQNVESDWPFAVIANLKGMLKYPFP 320
11 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 323 PFNPDKMLVKSIGDFV--KTEKLNKR-----ADGF----- 352
11 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 321 TTELTAKMTKVFQDFDGLQPKIKSQPIPESEODLVLYADNFDIYVDETRDYLYER 380
11 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 353 -GLWSSSDNAAHN-EQLAIEYVES 376
11 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 381 YAPMGCHKNKLAPTYEKAEYSDDS 406
11 : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 15
CHIT_CABEL
ID CHIT_CABEL STANDARD; PRT: 617 AA.
AC Q11174;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE PUTATIVE ENDOCHITINASE (EC 3.2.1.14).
GN Q04F6.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Nham M.;
RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF
CC N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
CC -1- SIMILARITY: BELONGS TO CHITINASE CLASS II (FAMILY 18 OF GLYCOSYL
CC HYDROLASES).
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U42835; AAA83586.1; -.
DR WormPep: Q04F6.3; CE03923.
DR InterPro: IPR002557; Chitin_binding.
DR InterPro: IPR001579; Chitinase. 2.
DR InterPro: IPR001223; Glyco_hydro_18.
DR Pfam: PF01607; Chitin_bind_2; 2.
DR Pfam: PF00704; Glyco_hydro_18; 1.
DR SMART: SM00494; ChIBD2; 2.
DR PROSITE: PS01095; CHITINASE_18; 1.
KW Hypothetical protein; Hydrolase; Glycosidase; Chitin degradation.
FT ACT_SITE 179 179 PROTON DONOR (BY SIMILARITY).
FT DOMAIN 435 478 THR-RICH.
SQ SEQUENCE 617 AA; 66857 MW; DDAID2AAAC0E54DA CRC64;

Query Match 5.3%; Score 104.5; DB 1; Length 617;
Best Local Similarity 21.1%; Pred. No. 5.3;
Matches 59; Conservative 41; Mismatches 86; Indels 93; Gaps 15;

58 YTPSVVSVNHL-----KDLNPNLVVMSFA--KMDLSYDSIESIVGSPLFLKSLIGLE 110
11 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
58 YFTNMAQYRQGRAKFVEDYTPGL-CTHILFAFGWMNAD-TYRAVDPAVL----- 106
11 : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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[illegible]

Search completed: May 8, 2002, 09:01:29
Job time: 207 sec


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Db 61 SWVSYNHNLKDLNPNLVNVMHSAKMDLSYDSIESIVGSPLLFSLIGLEYIGLNEYFND 120
Qy 121 AMNLKRPARDIIMLSLIGETYPSPSALNAVEKIANLVDELGPDIDVYEPNGSFD 180
Db 121 AMNLKRPARDIIMLSLIGETYPSPSALNAVEKIANLVDELGPDIDVYEPNGSFD 180
Qy 181 GLNDEKADFEVQYVTKLREYMCDDKLISISQSSNGALSCIGFNDPKKICMDDEAPYNSK 240
Db 181 GLNDEKADFEVQYVTKLREYMCDDKLISISQSSNGALSCIGFNDPKKICMDDEAPYNSK 240
Qy 241 YFNKPDVKELLRAAOMASAGAIYLMNNLKMDIMVFQVTNTNSTDYTKELDYSDY 300
Db 241 YFNKPDVKELLRAAOMASAGAIYLMNNLKMDIMVFQVTNTNSTDYTKELDYSDY 300
Qy 301 AYCGKRYVYIIMGFTLMEPTSPFNNDKMLVKSIGDFVTKENKLNKRGDFGLMSLSSD 360
Db 301 AYCGKRYVYIIMGFTLMEPTSPFNNDKMLVKSIGDFVTKENKLNKRGDFGLMSLSSD 360
Qy 361 NAAHNEOLAIEYVESLH 378
Db 361 NAAHNEOLAIEYVESLH 378

RESULT 2
Q9NJX8 PRELIMINARY; PRT; 323 AA.
ID Q9NJX8;
AC Q9NJX8;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CHITINASE (FRAGMENT).
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_Taxid=5833;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-20209408; PubMed-10744721;
RA Vinetz J.M., Valenzuela J.G., Specht C.A., Aravind L., Langer R.C.,
  Ribeiro J.M.C., Kaslow D.C.;
  "Chitinases of the Avian Malaria Parasite Plasmodium gallinaceum, a
  RT Class of Enzymes Necessary for Parasite Invasion of the Mosquito
  RT Midgut."
  J. Biol. Chem. 275:10331-10341(2000).
  CC -1- SIMILARITY: BELONGS TO CHITINASE CLASS II (FAMILY 18 OF GLYCOSYL
  CC HYDROLASES).
  CC EMBL: AF072442; AAF63209.1; -
  DR InterPro: IPR001579; Chitinase.2.
  DR InterPro: IPR002114; Pts_HPR_ser.
  DR PROSITE: PS01095; CHITINASE_18; 1.
  DR PROSITE: PS00589; Pts_HPR_SER; UNKNOWN.1.
  KW Glycosidase; Hydrolase.
  FT NON_TER 1
  FT NON_TER 323
  FT SEQUENCE 323 AA; 36502 MW; 9079ADEFE0F754D2 CRC64;
```

Query Match 85.5%; Score 1694; DB 5; Length 323;
Best Local Similarity 100.0%; Pred. No. 2.5e-111;
Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy 52 KGIIOGYPPSVYNHNLKDLNPNLVNVMHSAKMDLSYDSIESIVGSPLLFSLIGLEY 111
Db 1 KGIIOGYPPSVYNHNLKDLNPNLVNVMHSAKMDLSYDSIESIVGSPLLFSLIGLEY 60
Qy 112 IGLNEYNDAMNLKRPARDIIMLSLIGETYPSPSALNAVEKIANLVDELGPDIDV 171
Db 61 IGLNEYNDAMNLKRPARDIIMLSLIGETYPSPSALNAVEKIANLVDELGPDIDV 120
Qy 172 DYEPNGSFDGLNDEKADFEVQYVTKLREYMCDDKLISISQSSNGALSCIGFNDPKKICM 231
Db 121 DYEPNGSFDGLNDEKADFEVQYVTKLREYMCDDKLISISQSSNGALSCIGFNDPKKICM 180
Qy 232 DDEAPYNSKYFNKPDVKELLRAAOMASAGAIYLMNNLKMDIMVFQVTNTNSTDY 291
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Db 181 DDEAPYNSKYFNKPDVKELLRAAOMASAGAIYLMNNLKMDIMVFQVTNTNSTDY 240
Qy 292 VKKELDYSAAYGKRYDVYIIMGFTLMEPTSPFNNDKMLVKSIGDFVTKENKLNKRGD 351
Db 241 VKKELDYSAAYGKRYDVYIIMGFTLMEPTSPFNNDKMLVKSIGDFVTKENKLNKRGD 300
Qy 352 FGLMSLSDNAAHNEOLAIEYFV 374
Db 301 FGLMSLSDNAAHNEOLAIEYFV 323
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RESULT 3
Q9NJX9 PRELIMINARY; PRT; 587 AA.
ID Q9NJX9;
AC Q9NJX9;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE ENDOCHITINASE PRECURSOR (EC 3.2.1.14).
OS Plasmodium gallinaceum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_Taxid=5849;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-20209408; PubMed-10744721;
RA Vinetz J.M., Valenzuela J.G., Specht C.A., Aravind L., Langer R.C.,
  Ribeiro J.M.C., Kaslow D.C.;
  "Chitinases of the Avian Malaria Parasite Plasmodium gallinaceum, a
  RT Class of Enzymes Necessary for Parasite Invasion of the Mosquito
  RT Midgut."
  J. Biol. Chem. 275:10331-10341(2000).
  CC -1- SIMILARITY: BELONGS TO CHITINASE CLASS II (FAMILY 18 OF GLYCOSYL
  CC HYDROLASES).
  CC EMBL: AF064079; AAF63208.1; -
  DR InterPro: IPR001579; Chitinase.2.
  DR PROSITE: PS01095; CHITINASE_18; 1.
  KW Glycosidase; Hydrolase.
  SEQUENCE 587 AA; 67918 MW; 23D1ABA87DEBEE37 CRC64;
```

Query Match 32.0%; Score 635; DB 5; Length 587;
Best Local Similarity 37.4%; Pred. No. 1.4e-36;
Matches 129; Conservative 82; Mismatches 126; Indels 8; Gaps 5;

```
Qy 37 RKNPREIITKFEKSGKGIIOGYPPSVYNHNLK---DLNPNLVNVMHSAKMDLSYDSI 93
Db 89 RKNPQIILEYKRRKGIIAGTYGSMNSGDRAKHMDSNPMVSLIYAFARIMLYDVS 148
Qy 94 ESIYVSPLLFSLIGLEYIGLNEYFNDAAMLKRPARDIIMLSLIGETYPSPSALNA 153
Db 149 RPNRGORFLLRKHGLEVEYTGMMLEIRIRKVPDVIILSLIGETYP-MIDIEKIDY 207
Qy 154 VEKIANLVDELGPDIDVYEPNGSFDGLNDEKADFEVQYVTKLREYMCDDKLISISQ 213
Db 208 VDKILKLVNDFDLGDVIDMEPHGKFYLNELNFSNYIKLILNLTIRTEPKISISGS 267
Qy 214 SNGALSCIGFNDPKKICMDDEAPYNSKYFNK-PVKRELLRAAOMASAGAIYLMNNLKRD 272
Db 268 SNAALSCY--SGVASFCDESPNTKFLSQIETNKLHRAAAMLSAGPFINFNRAKE 325
Qy 273 MIDVVFQVTNTNSTDYTKELDYSAAYGKRYDVYIIMGFTLMEPTSPFNNDKMLV 332
Db 326 KIDLVFIOTYN-LETTNNDIMVWYLSHYLGKLYNTIILIGFSLHNRRGFSPEKNELL 384
Qy 333 KSIQDFVTKENKLNKRGDFGLMSLSSDNAHNEOLAIEYVESL 377
Db 385 ELVGKTIHDKQNNNRADGIGIMHLMFKRQLPTGSFVDIFLWNI 429
```

RESULT 4
Q48494 PRELIMINARY; PRT; 699 AA.

AC 048494:
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, last annotation update)
 DE CHITINASE.
 OS Kurthia zopfii.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 CC Bacillus/Staphylococcus group; Kurthia.
 OX NCBI_TaxID=1650;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ikeda S., Toyoda H., Matsuda Y., Ouchi S.;
 RT "DNA sequence determination of a chitinase gene chisH1 cloned from
 RT gram-positive bacterium Kurthia zopfii and its application to
 RT biological control of Powdery Mildew of Barley.";
 RL Submitted (Aug-1995) to the EMBL/Genbank/DBJ databases.
 CC -1 SIMILARITY: BELONGS TO CHITINASE CLASS II (FAMILY 18 OF GLYCOSYL
 CC HYDROLASES).
 CC EMBL: D63702; BAA09831.1; -.
 DR HSSP; P07254; ICTN.
 DR InterPro: IPR001579; Chitinase-2.
 DR InterPro: IPR003610; Chitin_bind3.
 DR InterPro: IPR003962; FcIII_repeat.
 DR InterPro: IPR001223; Glyco_hydro_18.
 DR InterPro: IPR001680; WD40.
 DR Pfam: PF00041; fn3; 2.
 DR Pfam: PF00704; Glyco_hydro_18; 1.
 DR PRINTS: PR00014; FNTYPEIIT.
 DR SMART: SM00495; ChitBD3; 1.
 DR SMART: SM00060; FN3; 2.
 DR PROSITE: PS01095; CHITINASE_18; 1.
 DR PROSITE: PS00678; WD_REPEATS_1; UNKNOWN_1.
 DR Glycosidase; Hydrolase; Repeat.
 KW SEQUENCE 699 AA; 73494 MW; 2AE9599A604BF513 CRC64;

Query Match 8.9%; Score 175.5; DB 2; Length 699;
 Best Local Similarity 20.1%; Pred. No. 0.00034;
 Matches 89; Conservative 59; Mismatches 109; Indels 185; Gaps 22;

55 IGGYPSWVS--NHNKLDNPNLVNHHMFAKMDLSYSIES----- 95
 46 IGGYPSWAGYGRNIVWDIDPT-KVTHINVAADICMGVHGNDPPSPNPVWTQNE 104
 96 -----IVGSPILFKSLIGLEYIG-----LNEYFNDAMLRKARPDIIIMLSL 137
 105 KSQTIWNPNGTIVLDGPDWID---TGKTFAGDWDOP IAGINIQNLKLIKINERLKITISV 161
 138 GGETYHPSSFDALNAV--EKIAN-LVDEL---GPDGIDVYE--PNSGFDGLNDEKAD 189
 162 GGMTWNSNRSDDVAATRAATREVFANSVDFLRKYNEPDGVDLDWEYVSGLDG-NSKRSQD 220
 190 --FVQYVTKLEPYMDDKLISISOSNGALSCIGFNDPKKICMDEAIVNSKYFKRPV 247
 221 KONYTILLSKIREKL-----DAAGAV-----DG 243
 248 KELLRAAOMASAGAIYLMN---NLKMDIMVVEQTFNNTN---STDSTVMKELYD 298
 244 KYLL---TIASGASTYVAANTELINIASIVDMINIMTDFGANGKQSAHALLN--YD 298
 299 SYA-----YGRKYD----- 308
 299 PAASAGVDPANTFNVAAGAGHLNAGVPAKLVLGVPFYGGWPGCAQAGNGYOTCTG 358
 309 -----YIIMGFTLMPSTP-----FNPNDKMLV-----KSIQDF 338
 359 GSSVGTWMEAGSDFYDLEINYNKNGYTRVWMDTAKVPLIYNASNKRFISTYDAESIG-- 416
 339 VKTENKLNKRRADGFGILMSLSD 360
 417 YKTAVIKSKGLGAGMEFWELSGD 438

RESULT 5
 ID 092N10 PRELIMINARY; PRT; 832 AA.
 AC 092N10:
 DT 01-MAY-1999 (Tremblrel. 10, Created)
 DT 01-MAY-1999 (Tremblrel. 10, last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, last annotation update)
 DE CHITINASE A.
 GN CHIA.
 OS Clostridium paraputrificum.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
 CC Clostridium.
 OX NCBI_TaxID=29363;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN-M;
 RA Morimoto K., Karita S., Kimura T., Sakka K., Ohmura K.;
 RT "Cloning, Sequencing, and Expression of the Gene Encoding Clostridium
 RT paraputrificum Chitinase ChIA and Analysis of the chi Transcription.";
 RL Submitted (MAR-1998) to the EMBL/Genbank/DBJ databases.
 CC -1 SIMILARITY: BELONGS TO CHITINASE CLASS II (FAMILY 18 OF GLYCOSYL
 CC HYDROLASES).
 CC EMBL: AB012764; BAA34922.1; -.
 DR InterPro: IPR001579; Chitinase-2.
 DR InterPro: IPR003610; Chitin_bind3.
 DR InterPro: IPR001223; Glyco_hydro_18.
 DR Pfam: PF00704; Glyco_hydro_18; 3.
 DR SMART: SM00495; ChitBD3; 1.
 DR PROSITE: PS01095; CHITINASE_18; 1.
 KW Glycosidase; Hydrolase.
 KW SEQUENCE 832 AA; 92586 MW; BB6FE9B04370478 CRC64;

Query Match 8.5%; Score 167.5; DB 2; Length 832;
 Best Local Similarity 24.9%; Pred. No. 0.0016;
 Matches 90; Conservative 50; Mismatches 130; Indels 91; Gaps 19;

9 FLVICLLCLLSTVYSVIEGHRARPEGRKRNPREIKTFKESG--KGIQGYPSWVSYN 66
 9 FLSTLLVALTSAGITVTSAR---EAKDNGOLANTNEKNDELKRIKIVGFEPN-AVS 63
 67 -----HNKLDN-PNLNVNHHMFAKMDLSYSI-----ESTVSPILFKSLT-- 107
 64 SEAGQYFNATDQLQMSLTIQYSFMAVDPSYTNKITLGDKHAAIEEDPFTGYDLSYNGKIYE 123
 108 ---GLEVIGLNEYFNDAMLRKARPDIIIMLSIGFT-----YHSSPDSALNA-VEKIA 158
 124 LDTSLPYKG--HFNVLQTKRKSPVDLLISVGGAGSRGFTYMLDTPAGINTFADSCV 180
 159 NLVDELGPDGIDVDEPNPSFDGLNDEKADFFVOYVTKLREYMCDDKLISISOSNGAL 218
 181 EPIRQYGFQVDIDFEYPSATQSQGNPDQDSEPRSRKLNRY--NLIKITLR----- 232
 219 SCIGFNDPKKICMDEAIPNSKYFPKPDYKKEKLLRAQMAS---AGAIYLLMNNLKMMD 275
 233 -----OKI--DEAA-----KADGKDYLLAAVYASPMVLGV--SDNSYAKYLD 272
 276 MVEYOTFN-----YTNSDSTVMKELYD-----SYAY-GKKYDVIIM 313
 273 FLVSMSYDIHGGMNEVEHLAGIYRNAEDRETYVAOIMPLCDMAVRIYRGVLPSEKILM 332
 314 G 314
 333 G 333

RESULT 6
 ID 09KHB3 PRELIMINARY; PRT; 717 AA.
 AC 09KHB3:
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, last sequence update)

DT 01-JUN-2001 (Tremblrel. 17, last annotation update)
DE CHITINASE.
GN CH11.
OS Bacillus circulans.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=1397;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-C-2;
RA Wang Y.L., Wang H.Y., Qin M., Zhang Y.Z.;
RT "Nucleotide sequence of a chitinase gene (ch11) from Bacillus
circulans C-2."
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF265220; AAF74782.1;
DR InterPro: IPR001579; Chitinase_2.
DR InterPro: IPR003610; Chitin_bind.
DR InterPro: IPR003962; FnIII_repeat.
DR InterPro: IPR003961; Fn_III.
DR InterPro: IPR001223; Glyco_hydro_18.
DR Pfam: PF00041; fn3; 2.
DR Pfam: PF00704; Glyco_hydro_18; 1.
DR PRINTS; PR00014; FMYPEPIL.
DR SMART; SM00495; CHBD3; 1.
DR SMART; SM00060; FN3; 2.
DR PROSITE; PS01095; CHITINASE_18; UNKNOWN_1.
DR Hydrolyase; Repeat.
KW Hydrolyase.
SQ SEQUENCE 717 AA; 76118 MW; BB0B019CDE72C198 CRC64;

Query Match 8.1%; Score 160.5; DB 2; Length 717;
Best Local Similarity 22.8%; Pred. No. 0.004;
Matches 105; Conservative 65; Mismatches 143; Indels 147; Gaps 27;

QY 11 VILLICLLSTTVYS-VIEGHRARPGESRKNPRILTFKESGKIIIGYPSWVSYN--N 66
DB 16 VLLGLVLLSTTVIPSETIOSRTAEDADYK-----IVGYPMAAAYGRN 59
QY 67 HNLKDLNPNLVNVMHSAKMDLSYDSIES-----IV 97
DB 60 YNTYDIDPT-KVTHINAFADICWNGIHGNDPSPNPVTWSCNKSQITINPCTIVL 118
QY 98 GSPLL--FKSLIG----LEYGLNEFYENDAMNLRKRPDIIMLSLGETYHPSEDSAL 151
DB 119 GDMWIDRKGOFAGDTWOPAG--NINQLNKLKOVNPNLTIIISIGGWTSMNRESDVA 175
QY 152 NAV--EKIAN-LYDEL---GPDGIDV--DYEPNGSPDLNKEKAD--FEQVYTKLREY 201
DB 176 TSAITREVFANSADVFLKRYNFDGVDLNMWEPVSGLDG--NSKRPEDKONTYLLSKIREK 234
QY 202 M-----CDDK--LISISQ-----SSNGALSCIG-----FNDPKKICMDEAP 236
DB 235 LDAEAENVGKEYLLTISGASPTAANTDELANISYDVIMINIMYDFGCAQNKISAHNAP 294
QY 237 YN-----SKYFNKPDVKKELLRQAQMASAGAIYLMNVL--KMIDMVF-- 278
DB 295 LNADPAASAGVDPDSNFTN-----YAAGQGHILNAGVPAKLVLGPEFYGR 340
QY 279 -----VQTFN--YTNGTSDTVMKELDYSAVYGGKKYDYVILMFETLMEPT--PF--N 325
DB 341 GMDGCAQADNGOYOTCGGGSSIGTWEAGSEFDYDLNAYINKNGYTRYWMDTAVVPLYN 400
QY 326 PNDKMLV-----KSIGDFVTKENLKNRAGDGLMSLSD 360
DB 401 ASKRFISYDAESIGH--KTAATKSKGLGAGMFWELSGD 438

RESULT 7
ID 097403 PRELIMINARY; PRT; 405 AA.
AC 097403;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, last sequence update)

DT 01-JUN-2001 (Tremblrel. 17, last annotation update)
DE CHITINASE PRECURSOR (EC 3.2.1.14).
OS Phaeodon cochleariae (Mustard beetle).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
OC Cucujiformia; Phytophaga; Chrysomeloidea; Chrysomellidae;
OC Chrysomellinae; Phaeodon.
OX NCBI_TaxID=80249;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-GUT;
RA Girard C., Jouanin L.;
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
CC -1 SIMILARITY: BELONGS TO CHITINASE CLASS II (FAMILY 18 OF GLYCOSYL
HYDROLASES).
DR EMBL; Y18011; CAAT7014.1;
DR HSSP; P07254; ICTN.
DR InterPro: IPR001579; Chitinase_2.
DR InterPro: IPR001064; Crystallin.
DR InterPro: IPR001223; Glyco_hydro_18.
DR Pfam: PF00704; Glyco_hydro_18; 1.
DR PROSITE; PS01095; CHITINASE_18; 1.
DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
KW Glycosidase; Hydrolyase; Signal.
KW SIGNAL 1 20 POTENTIAL.
FT CHAIN 1 405 CHITINASE.
SQ SEQUENCE 405 AA; 44995 MW; 11E900AFA66272AD CRC64;

Query Match 7.9%; Score 156.5; DB 5; Length 405;
Best Local Similarity 20.2%; Pred. No. 0.0033;
Matches 74; Conservative 63; Mismatches 114; Indels 115; Gaps 15;

QY 9 FLVICLLCLSTVYSVIEGHRARPGESRKNPRILTFKESGKIIIGYPSWVSYN-- 66
DB 6 FISFVLLTIRSS-ISTV-----SGRNV-CITFASVYIRPG 40
QY 67 --HNLKDLNPNLVNVMHSAKMDLSYDSIESIVGSPLEKSLIGLEYGLNEFYENDAMN 123
DB 41 NGLFVSNIEEDL-CTHINFAFIGHEDGTINIDK--WESDDGKYHG--FRLLD 92
QY 124 LKRAPDIIMLSLIG-----ETHPSEDSAL--NAVEKIANLYDELGPDGIDVDEYN 176
DB 93 LNSHPSLKYLVSMGNEGKTSKYAADVLRKTLANNVGAFTROYGDFGDIOMEYR 152
QY 177 GSPDLNKEKADFFVQVTKLREYM--CDDKLISOSSNGALSCIGFNDPKKICMDEA 235
DB 153 GSREGSNVTTDKDNFVALLIEDLSAVLHPKGLLRAAAGVERIDGFDVPR----- 204
QY 236 PYNKRYFNKPDVKKELLRQAQMASAGAIYLMNVLKMDID-MVF----- 278
DB 205 -----VNEILDMINVMYDFHGFEPVGHLSPL 233
QY 279 -VQTFNITNSTDSTVMKELYSAVYGGKKYDYVILM-----FTLMFSTFPNPDMA 330
DB 234 HASSIDYENGNATMTATATGIRKWIYKASPEKINMGATYGRSFTLKDNL-----NTOL 288
QY 331 LVKSIG 336
DB 289 YAPNVG 294

RESULT 8
ID 007088 PRELIMINARY; PRT; 635 AA.
AC 007088;
DT 01-JUL-1997 (Tremblrel. 04, Created)
DT 01-JUL-1997 (Tremblrel. 04, last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, last annotation update)
DE CHITINASE.
GN CH1.
OS Bacillus thuringiensis.
OS Bacteria; Firmicutes; Bacillus/Clostridium group;

OC Bacillus/Staphylococcus group; Bacillus.
 OX NCBI_TaxID=1428;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sonngay S., Panbangred W.;
 RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO CHITINASE CLASS II (FAMILY 18 OF GLYCOSYL
 HYDROLASES).
 DR EMBL: U89796; AAB58579.1; -.
 DR InterPro: IPR001919; CBD_2.
 DR InterPro: IPR001579; Chitinase_2.
 DR InterPro: IPR003861; FN_III.
 DR InterPro: IPR001223; Glyco_hydro_18.
 DR Pfam: PF00553; CBD_2; 1.
 DR Pfam: PF00041; fn3; 1.
 DR Pfam: PF00704; Glyco_hydro_18; 2.
 DR SMART: SM0060; FN3; 1.
 DR PROSITE: PS00178; AA_TRNA_LIGASE_1; UNKNOWN_1.
 DR PROSITE: PS01095; CHITINASE_18; 1.
 KW Glycosidase; Hydrolase.
 SQ SEQUENCE 635 AA; 71096 MW; 72D970E9DB1CC3AD CRC64;

Query Match 7.5%; Score 149; DB 2; Length 635;
 Best Local Similarity 18.7%; Pred. No. 0.021;
 Matches 85; Conservative 76; Mismatches 127; Indels 166; Gaps 19;
 OY 6 KYSFVILCLCL--LSYVSVEIGHRAPGESRKNPREIKTFKESGKIIOGYPSW 62
 DB 7 KFTLLLSLLEFLPLFTNFITPNALADSPKOSK-----IVGYFPSW 50
 OY 63 VSY--NHNKLDLNPMLNVHMSFAKMDLSYDSIESIVSP-----LIFKSLI--- 107
 DB 51 GYGNANYOVADIDAS-KLTLNLYAFADICWNGKH--GNPFSSNQINKLDCRDLVYHC 106
 OY 108 -----GLEYGLENE-----YENDANLKRARPDITMLISL 137
 DB 107 KIKVNGNLTGLVGENHGLMLPNRILOQTTEWEDCKYARGNFGELRKAKYPHLEKTIISV 166
 OY 138 GGETYHPSFSDALNA-----VEKIANLYDELGFSDIVDYE-----PNSFSDGLND 184
 DB 167 GGMTSARNSPDMADKTRKYPFAESTVAFPLPAYGFDVLDMEYGVETIFEGST---RP 223
 OY 185 KEKADFVQVYTKLEHYMCDDLKISISQSSNGALSCIGFNPDKKICMDDEAPYNSKFNK 244
 DB 224 EDKQKFTL-----LLOELRNALNKAGAECKOYLLTIPSGASQRYADH 266
 OY 245 PDVKK-----ELRAQMASNGAIYIMNNIKMDIADVFQTFN----- 283
 DB 267 TELKRTISOYSTIGLISHMISTADGKLL-----TIMOLYIGSNDPANTNFEYVDGAINV 320
 OY 284 YTNSTDS-----TVMKELDYSAVYKKYDYVILMGFTLFPSTPEPNCKMLVK 333
 DB 321 YTNNEVSLPLPQCCKPLDLVLVKELOG-----PISQKHTPEPT 357
 OY 334 SIGDFVKTENLKRADGFGI--WLSISSDMAANE 366
 DB 358 NVKNIVT-----NKNNSNVQLNMWTVSTDNVGYTE 387

RESULT 9
 O9RG51 PRELIMINARY; PRT; 496 AA.
 ID O9RG51
 AC O9RG51
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, last annotation update)
 DE CHITINASE.
 GN CH141.
 OS Bacillus circulans.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 OC Bacillus/Staphylococcus group; Bacillus.

OX NCBI_TaxID=1397;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN-NO. 4.1;
 RC Thepouyorn A., Wiat C.;
 RT "Chitinase-encoding gene from Bacillus circulans";
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO CHITINASE CLASS II (FAMILY 18 OF GLYCOSYL
 HYDROLASES).
 DR EMBL: AF154827; AAF23368.1; -.
 DR HSSP: P07254; ICTN.
 DR InterPro: IPR001579; Chitinase_2.
 DR InterPro: IPR001223; Glyco_hydro_18.
 DR Pfam: PF00704; Glyco_hydro_18; 1.
 DR PROSITE: PS01095; CHITINASE_18; 1.
 KW Glycosidase; Hydrolase.
 SQ SEQUENCE 496 AA; 55969 MW; 25E7D2AF0F213649 CRC64;

Query Match 7.5%; Score 148.5; DB 2; Length 496;
 Best Local Similarity 21.5%; Pred. No. 0.016;
 Matches 105; Conservative 72; Mismatches 138; Indels 173; Gaps 28;
 OY 7 YSFLVILCLCLSTVYVIEGHRAPGESRKNPREIKTFKESGKI-IOGYPSWVS 65
 DB 15 FSFIFVMLLS-----LSFVNGEVAK-----ADSKNKKIIGYPSWAV 53
 OY 66 NHNLK--DLNPLNVHMSFAKMDLSYDS-----IES----- 95
 DB 54 GRNFYWMMDVS-KVSHINLYAFADICWGRGNPPTGPNPOTWSCODENGYIDAPNGTI 112
 OY 96 IVGSPL--FNSLIG--LEYIGLEYNDAANLKRARPDITMLISGGEYHPSFDSA 150
 DB 113 VMGDWDIAQNSPNQVDDEPIRGN--FKQLLKLKSHPLKTFISVGWFSNRFSDVA 170
 OY 151 LNAVER---IANLDEL---GFDGIDVYE--PNSFSGLN---DKEKADFVQVYTK- 197
 DB 171 ADPVARGNFASAVEFLKRYGFDVLDMEYGVSGLPGNSRPRDKRNYTLLOECVKN 230
 OY 198 -----LREYMCDDLKISISQSS-----SNGALSCIG----- 222
 DB 221 LMLQKRTAREYLITIASGASPEYVSNTELDKIAOTVIMINIMTYDFNGQSIANHAP 290
 OY 223 -FNDE--KKICMDDEAPYN---SKYFNKPDYKELL-----RAAQMASAG- 262
 DB 291 LEYDRAKEAGVPAETNIENITVYKRYKAGYKGLVIGTPEYGRGSGSGGGEYQ 350
 OY 263 -----AYILMNNK-----DMLDMVFVQTFNTNSTDSVYMKEL 296
 DB 351 KCGPAKEGTWENGVDYFSDLEKNYVNGYKRYWMDQAKVPFL--YNAENGFTI----- 403
 OY 297 YDSYAYYKRYDYVILMGFT--LMFPSTPEPNCKMLVYSIGDF--VTE--NKLNRRA 349
 DB 404 YDDESGFGRKNDFTIRANLSCAMFWDFSGDSNPTLLNKLAEFKCTCTEAIARNLHH- 462
 OY 350 DGFGLMSL 357
 DB 463 ----LMMV 466

RESULT 10
 O9FAC8 PRELIMINARY; PRT; 674 AA.
 ID O9FAC8
 AC O9FAC8
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, last annotation update)
 DE CHITINASE B.
 GN CH1B.
 OS Bacillus cereus.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 OC Bacillus/Staphylococcus group; Bacillus.
 OX NCBI_TaxID=1396;

[1]
 RN SEQUENCE FROM N.A.
 RP STRAIN-CH;
 RA Mabuuchi N., Araki Y.;
 RT Chitinase.
 RL Submitted (Apr-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB041932; BAB16891.1;
 DR InterPro: IPR001919; CBD_2.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR001223; Glyco_hydro_18.
 DR InterPro: IPR001412; RNA-syn_1.
 DR Pfam: PF00553; CBD_2; 1.
 DR Pfam: PF00441; fn3; 1.
 DR Pfam: PF00704; Glyco_hydro_18; 1.
 DR SMART: SM00060; FN3; 1.
 DR PROSITE: PS00178; AA_TRNA_LIGASE_I; UNKNOWN_1.
 KW Hydrolyase.
 SQ SEQUENCE 674 AA; 74262 MW; 66BE9FE80D680561 CRC64;

Query Match 7.4%; Score 146.5; DB 2; Length 674;
 Best Local Similarity 17.1%; Pred. No. 0.035;
 Matches 88; Conservative 82; Mismatches 117; Indels 227; Gaps 20.

QY 6 KYSLVYLCLCL--ISTYVVEIGHRRAPGESRKNPREIITKFKESGKIIGYPSW 62
 DB 5 KFTLLSLLLFLPLFLNFINPMLALADSPKQSO-----IVGTFPSW 48
 QY 63 VSR--NINLKDLPNPNLVNHSFAKMDL-----SYDSIESIVGSPL 101
 DB 49 GYVGRNVQVADIDAS-KLTLNVAFAADICWNGKHNPSTHDPNPKQYWNKES--GYPL 105
 QY 102 LFFSL-----IGLEYIGLNEY-----FNDAMNLRKARPDITMLIS 136
 DB 106 QNKEVPEVGTLYLGPMDADYTSYSGSGTTWEDCKYACNGFGLKRLKAKYPIHLKTTIS 165
 QY 137 LGGETYHPSSEFSAIINAVEKIANLVD-----LGFQDIDVDE-----PNSGSDG 181
 DB 166 VGGWTW--SNRFSMDADEKTRKFAESTVAFRLAYGFGDVLDMVEYGVETIPGVS-- 221
 QY 182 LNDKERADFVQYVYTKLREYKCDKLISISOSNGALSICGFNDPKKICMDEAPYNSKY 241
 DB 222 -RPEDKONFL-----LQDVNRNALNKAQAEQKQYLLTLTASASQRY 263
 QY 242 FNRPDYKELLRAQAQASAGAIYLMNLRKMDIMVYQYENY-----TJNSTDSTVKE 295
 DB 264 ADITELKK-----ISQILDMINIMTYDFHGGWATSNHNAALYKD 303
 QY 296 LYDSA-----YGGKRY----- 307
 DB 304 PNDPAANTNFHVDGAINVYTNVGVVDKLYGVFPYGRGKSCGKENGQYQCPKPSDG 363
 QY 308 -----DYVILMGFTLMPPST-----PNNP 326
 DB 364 KLASKGWDDYSTGDTGVYDGLAANTVKNRGNFVRYWNTAKVYLYLNATGTTFISYDD 423
 QY 327 NDKMLVKSIGDFYTKENKLRADGFLMSLSD 360
 DB 424 NESMKYKT--DYIKT-----KGLNGAMFWELSGD 450

RESULT 11
 ID 09KT32 PRELIMINARY; PRT; 1088 AA.
 AC 09KT32;
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE CHITINASE, PUTATIVE.
 GN VC1073.
 OS *Vibrio cholerae*.
 OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; *Vibrio*.
 OX NCBI_TaxID=666;

[1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=EL TOR N16961 / SEROTYPE O1;
 RX MEDLINE-20406833; PubMed-10952301;
 RA Heidelberg J.F., Eilen J.A., Nelson W.C., Clayton R.A., Gwin M.L.,
 RA Dodson R.J., Hatt D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
 RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
 RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragol I., Sellers P.,
 RA McDonald L., Uitterback T., Fleischmann R.D., Niernan W.C., White O.,
 RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
 RA Fraser C.M.;
 RT "DNA sequence of both chromosomes of the cholera pathogen *Vibrio*
 RT *cholerae*."
 RL Nature 406:477-483(2000).
 CC -I- SIMILARITY: BELONGS TO CHITINASE CLASS II (FAMILY 18 OF GLYCOSYL
 CC HYDROLASES).
 DR EMBL: AE004188; AAP94232.1; -.
 DR TIGR: VC1073; -.
 DR InterPro: IPR001579; Chitinase_2.
 DR InterPro: IPR003610; Chitin_bind.
 DR InterPro: IPR001223; Glyco_hydro_18.
 DR Pfam: PF00704; Glyco_hydro_18; 2.
 DR Pfam: PF00495; ChitBD3; 1.
 DR SMART: SM00495; ChitBD3; 1.
 DR PROSITE: PS01095; CHITINASE_18; 1.
 KW Complete proteome; Glycosidase; Hydrolase.
 SQ SEQUENCE 1088 AA; 118409 MW; 34373BA5FA4089C CRC64;

Query Match 7.4%; Score 146.5; DB 2; Length 1088;
 Best Local Similarity 23.6%; Pred. No. 0.07;
 Matches 79; Conservative 60; Mismatches 103; Indels 93; Gaps 21;

QY 39 NPREITKFKESGKIIGYPSWSYVHNK-----DLNPNLVNHSFA-----KMDL 88
 DB 383 HPRIT-----GYTSMRTKNGLPATLAGDLPWEKLTINAFASINKSDF 429
 QY 89 SYDSIESIVGSPLFKSLIGLE-----YIGLNEYFNDAMNLRKARPDITMLISIGS-E 140
 DB 430 SMQVDD--ATKRMWENVPGAEEMPSPLYG--HFNLISFKKQYDVTLLISVGMAE 484
 QY 141 T--YHPSFSDA-----LNAVEKTA-NLYDELGEGDIDVDE-PNSGFDGLNDEKA 188
 DB 485 TGGFYPMTTDLASGVNNEGIRKNSAVDFIRQYDGDVIDEYPSMKDSGN--PV 541
 QY 189 DEFQYVYKLRMYMDOKLISISOSNGALSICGFNDPKKICMDEAPYNSKYFNKPDV 248
 DB 542 DF--EQSKCKGQMDNVMVMTLKR-ALDKAGEDEGRKIMLTIASP--SSAT----- 590
 QY 249 KELLRAQAQASAGAIYLMNLRKMDIMVYQYENY-----YJNSTDSTVM 293
 DB 591 --LRGMQDFA-----MQVLDVYVNIYSYDLHGTWNEFVGPQALFDGKDAELA 638
 QY 294 K-ELYDSYAYGKKYDYIIMGFTLMPPSTPFENN 327
 DB 639 KWGYVTTAETGYGIGY--LNAQWTHFFRGAFKPS 670

RESULT 12
 ID 09P401 PRELIMINARY; PRT; 560 AA.
 AC 09P401;
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE CHITINASE.
 GN CT51.
 OS *Ajellomyces capsulata* (Histoplasma capsulatum).
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Onygenales; Onygenaceae; *Ajellomyces*.
 OX NCBI_TaxID=5037;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=G217B;

RA Thomas P.W., Cole G.T.;
RT "Identification and functional characterization of a chitinase from
RT Histoplasma capsulatum: protein purification and isolation of genomic
RT and full-length cDNA."
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO CHITINASE CLASS II (FAMILY 18 OF GLYCOSYL
CC HYDROLASES).
DR EMBL: AF159366; AAF80370.1; -
DR InterPro: IPR001579; Chitinase_2.
DR InterPro: IPR001223; Glyco_hydro_18.
DR Pfam: PF00704; Glyco_hydro_18; 1.
DR PROSITE: PS01095; CHITINASE_18; 1.
KW Glycosidase; Hydrolase.
SQ SEQUENCE 560 AA; 61347 MW; EF34B32ED9B064E2 CRC64;

Query Match 7.4%; Score 146; DB 3; Length 560;
Best Local Similarity 21.7%; Pred. No. 0.029; Indels 122; Gaps 22;
Matches 89; Conservative 56; Mismatches 143;

QY 32 RPSGRKRPRIITFKESGKIIQGYPSWVSY--NHNLKDLNPNLVHMSFAKMDLS 89
DQ 140 RPSPPSPSPSHMSS--PDGYKSIY--YVNMATYARNYPODL-PVKKLTHVLA----- 190
QY 90 YDSIESIYGSFLKSLIGLE-----YIGLNEY--FNDANMLRKARPDITMLSLG 138
DQ 191 FANVRAESGEVFLDTADYDKHPTDSWSEFGNNVGVCKQLFLKKONRHLKVLSTIG 250
QY 139 GETYHPSFSDSALNA-----VEKIANLVDELPGDIDVYE--PNSGFDLNRKADF 190
DQ 251 GWITSP-HFGAAYSTPAARKTFADSATOLNLTGPDGADIMEYF-----KDEEAKS 302
QY 191 FVOYVTKREYKCDKLISISQSSNGALSCIGFNDPKRICMDDEAPYNSKYFNKPDVKE 250
DQ 303 LVELLKTRE-----VLDLAGKD-RRLFLTVACPAQRQFEK----- 339
QY 251 LLRAQAASAGAIYLLNNKMDIMFVOTFNTNSTDSIV----- 292
DQ 340 -LRREMT-----PYLDFNYLMAYDYSGSWDITAGHOSNIEISKSRNSTPF 385
QY 293 -MKELYSYAYGKRYDVIIIMGFTLM-----FPSTPPNPN--DKMLVKSIGDF--- 338
DQ 386 STRAIVDYVGVGKPSKLLGMPLYGRTPADTDGPGTPRHGGGCGSFERGIWDYKSL 445
QY 339 -----VTEENKLNKRDGFGLS-----LSSDNAHNAQDLAEYFVE 375
DQ 446 PKVGAVEHIDLEKGGCG-ASMSYDASSRTMISYDNVAMVE-KTKYTIQ 493

RESULT 13
Q9HEW6 PRELIMINARY; PRT; 493 AA.
AC Q9HEW6;
DT 01-MAR-2001 (TREMblrel. 16, Created)
DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE CHITINASE.
GN CTS2.
OS Ajiellomyces capsulata (Histoplasma capsulatum).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Onygenales; Onygenaceae; Ajiellomyces.
OX NCBI_Taxid=5037;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-G217B;
RA Specht C.A., Benfield B.B., Garcia J.J.;
RT "Identification of bacteria-like chitinases in fungi."
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF315588; AAG41982.1; -
DR InterPro: IPR001223; Glyco_hydro_18.
DR InterPro: IPR000531; TonB_box.
DR Pfam: PF00704; Glyco_hydro_18; 1.
DR PROSITE: PS00430; TonB_DEPENDENT_REC_1; UNKNOWN_1.

SQ SEQUENCE 493 AA; 53623 MW; E9C420F2790D9179 CRC64;

Query Match 7.2%; Score 142; DB 3; Length 493;
Best Local Similarity 22.2%; Pred. No. 0.046;
Matches 70; Conservative 43; Mismatches 102; Indels 100; Gaps 15;

QY 58 YPSWVSY--NHNLKDLNPNLVHMSFAKMDLSYDSIESIYGSFLKSLI----- 107
DQ 101 YVNMATYGRNYQPODL-PAKLTHTVLA-----FANVHGCTGEVYLLINDYNADTDKHYPT 154
QY 108 -GLEIYGLNEY--FNDANMLRKARPDITMLSLGETYHPSFSDSALNAVERKIALVYD-- 162
DQ 155 DSWEDVGNVYGVCKQLFLKKONRHLKILISIGWY--SSNFGAATAANRAHFAFTA 213
QY 163 -----ELGFDGIDVYE--PNSGFDLNRKADFVQYVTKREYKCDKLISISQSSNG 216
DQ 214 TKMLMDGFDGLDIMEYF-----NDEEAKNVELLKTRE-----KDELSKN--- 258
QY 217 ALSCTGFNDPKRICMDDEAPYNSKYFNKPDVKKELRAQAASAGAIYLLNNKMDIM 276
DQ 259 -----RKFLTVACPAQRQFEK-----LRLEMT-----PYLDF 288
QY 277 VFQTFNTNSTDSIV-----MKELYSYAYGKRYDVIIIMGFTL 317
DQ 289 YNLMAVYDAGSMDYVAGHANLEVSQPSKSTPYSTEAALDYIGVGEVASKMILGMP 348
QY 318 M-----FPSTPF 324
DQ 349 YGREPADTDGPGTTP 363

RESULT 14
P94339 PRELIMINARY; PRT; 604 AA.
AC P94339;
ID P94339;
DT 01-MAY-1997 (TREMblrel. 03, Created)
DT 01-MAY-1997 (TREMblrel. 03, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE CHITINASE (EC 3.2.1.14) (CHITODEXTRINASE) (1,4-BETA-POLY-N-
DE ACETYLGLUCOSAMINIDASE) (POLY-BETA-GLUCOSAMINIDASE).
GN CHT.
OS Bacillus licheniformis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_Taxid=1402;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-TP;
RA Tautimavanich S., Panbangred W.;
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF N-
CC ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
CC -1- SIMILARITY: BELONGS TO CHITINASE CLASS II (FAMILY 18 OF GLYCOSYL
CC HYDROLASES).
DR EMBL: U71214; AAB47847.1; -
DR HSP: P07254; ICTN.
DR InterPro: IPR001579; Chitinase_2.
DR InterPro: IPR003610; Chitin_bind3.
DR InterPro: IPR003962; Phitl_repeat.
DR InterPro: IPR001223; Glyco_hydro_18.
DR Pfam: PF00041; fn3; 1.
DR Pfam: PF00704; Glyco_hydro_18; 2.
DR PRINTS: PR00014; FMYXPELIT.
DR SMART: SM00495; ChEBD3; 1.
DR SMART: SM00060; FN3; 1.
DR PROSITE: PS01095; CHITINASE_18; 1.
KW Glycosidase; Hydrolase; Repeat.
SQ SEQUENCE 604 AA; 66837 MW; 65B39258444BB3D2 CRC64;

Query Match 7.2%; Score 142; DB 2; Length 604;

	Best Local Similarity	21.6%;	Pred. No.	0.062;	Mismatches	137;	Indels	162;	Gaps	26;
OY	7 YSEVLICCLCSTLSTVSYVIEGHRARPGESRKNPREILITKFEKSGKI-IGGYPSWSY	65								
Db	15 FSIFFVMLLS-----LSFVNGEAVK-----ADSGKNKYIIIGYPSWGA	53								
OY	66 NNNLK--DLNPLNLNVHMSFAKMDSLSDS-----IES-----95									
Db	54 GRNFQWMWDVS-KVSHLVAFADICWGEGRGNDPPTGNPQTWSCODENGVIDAPNGTI	112								
OY	96 IVGSPLL-FKSLIG---LEYGLMEFYEDAMNLKRAPPDIIMLSIGETYPSPFSDA	150								
Db	113 VMGDPMIDAQRSNPDGWDEPIRGN--FRQLKLTKSHHLTFLISYGWTWSNRFSDVA	170								
OY	151 LNAVER---IANLVDEL--GFDGIDVDYE-PNGSFGLN---DKEADEFFVOYVKL	198								
Db	171 ADPVARGNFASAVEFLRKRYCGDYLDWEYEVSGLPNSRPDEPKRNVTLLQEVRRK	230								
OY	199 -----REVM-----CDCKLS-----ISOSSNALSCIG-----222									
Db	231 LDAEAKDGEYLLFTIAGSADRIVYSNTELDIAOTVWININITYDFNGWOSISAHNAA	290								
OY	223 -FNDE-KKICDDDEAPYN---SKYFNKPDKY-----KELLR	253								
Db	291 LEYDFKAEAGVPNAETNYENTVYRKYKAGVGOKVLGPFPYEGAGAVNPATENIR	350								
OY	254 AAQMASAGA-----ITYLMNN-----LKDMDIVVQTFPNNTNSDSIVMKEL	296								
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OY	297 YDSYAYGKKKYDYVIIMGFT-LMFPSTPPNPMDKMLVKSIGD	337								
Db	404 YDDSGFGHKDTFIKANGLSGAMFDFSGDSNRITLKLALAD	445								
RESULT	15									
P96168										
ID AC	P96168	PRELIMINARY:	PR:	729	AA.					
CC	P96168									
OC	NCBI_TaxID=669;									
NN	[1]									
RP	SEQUENCE FROM N.A.									
RC	STRAIN-BB7;									
RX	MEDLINE=98274739; PubMed=9611805;									
RA	SVt11 A.U., Kitchen D.L.;									
RT	"A chitin-binding domain in a marine bacterial chitinase and other									
RT	microbial chitinases: implications for the ecology and evolution of									
RT	1,4-beta-glycanases.";									
RL	Microbiology 144:1299-1308(1998).									
DR	EMBL: U81496; AAC64383.1;									
DR	InterPro: IPR001579; ChitInase_2.									
DR	InterPro: IPR001638; SBP_bac_3.									
DR	InterPro: PS0103610; Chitin_bind.									
DR	PROSITE: PS01095; CHITINASE_18; UNKNOWN_1.									
DR	PROSITE: PS01039; SBP_BACTERIAL_3; 1.									
DR	SMART: SM00495; ChEBD3; 2.									
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Query Match	7.0%	Score 139;	DB 2;	Length 729;
Best Local Similarity	20.5%	Pred.	No. 0.13;	
Matches	83;	Conservative	60;	Mismatches 135; Indels 126; Gaps 20;
QY	19	LSTYSVTEGHRARGESKRNPRELIKTFKESGKITDGYISWV---	SYNH-----NL	69
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Db      11 VSVGLAASGAVYANGSDMTNP-----DSGVVVGYYQNMCCDGGYGCGNAPCVTL    60
Oy      70 KDLPNLNVAVHNSKPAKMDLSTDSIESIVGSPLFKSLIGLEYIGLN--VFNDAMNTPKA   127
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Db     61 DEVNEMYNIVNNSEMKV--YDVADGRIPTEKLDP-----VGISEOFLDOVSLENLKQ    111
Oy     128 RPDIMILSIGEFYHPSPFSALNA-VKTAANIYDELGFPGDIVDYEPNGSFGDLNKE   166
        :|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db     112 GRSV--LIATLGADAHAVELETFGERAFADEITRLTERYGFGFGLIDLE-QAAVTANNOQT   168
Oy     187 KADFVVQVYVTKLRXYMCEDKLTSISOSSNGALSCIGFNPKICOMDEAPNYSKFNKP    246
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Db     169 VIPDLAKLVKD-HRAEGKNFLT-----MAFEPP-                          198
Oy     247 VKELLRAQAASAGAIYLMNNIKMDIMWVYOTFN-----YTNSTDSTM    293
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Db     199 -----LTGGKYVPYIDNLEGYVDIMINPQFYNGDGDIWDCVMIAQNND---    244
Oy     294 KELYSYAYYCKRDYVIINGFTLMFPSTPN--PNDKML--VKSIDD-----PVKTENK   344
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Db     245 -ELKEEFTY-----IDSLSLNGTGFHKIAPHOKLVAFGPSSIDAATAATGFWKEPOD   294
Oy     345 LNKRAD-----GFLMSLSD-----NAAHNLEOLAEY    372
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Search completed: May 8, 2002, 09:01:10
Job time: 218 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 7, 2002, 11:49:39 ; Search time 2197.42 Seconds
(without alignments)
10827.913 Million cell updates/sec

Title: US-09-579-383-1

Perfect score: 1137
Sequence: 1 atgaattaccgtaaata.....tcgtgaagcctgcactaa 1137

Scoring table: IDENTITY_NDC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 segs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:*
1: gb_da:*
2: gb_hcg:*
3: gb_in:*
4: gb_cm:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_da:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_or:*
21: em_ov:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_hcg_hum:*
31: em_hcg_inv:*
32: em_hcg_other:*
33: em_hgtgo_inv:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB ID	Description
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1	1137	100.0	1137	3	AF172445	AF172445 Plasmodium
2	636.2	56.0	245802	2	AC006279	AC006279 Plasmodium
3	550.4	48.4	1325	3	AF072442	AF072442 Plasmodium
4	171.6	15.1	1764	12	AF216703	AF216703 Synthetic
5	104.2	9.2	2500	3	AF064079	AF064079 Plasmodium
6	70.2	6.2	2562	3	PBE305256	AJ305256 Plasmodium
7	43.8	3.8	1141	6	AX083744	AX083744 Sequence
8	43.6	3.8	1624	3	AB022908	AB022908 Apis mell
9	41.8	3.7	1141	6	AX083744	AX083744 Sequence
10	40.2	3.5	119526	9	AL359267	AL359267 Human DNA
11	40.2	3.5	158515	2	AC021404	AC021404 Homo sapi
12	40.2	3.5	158553	8	AC084884	AC084884 Oryza sat
13	40	3.5	166757	8	AC098565	AC098565 Oryza sat
14	39.4	3.5	160294	2	AC106505	AC106505 Rattus no
15	38.8	3.4	3867	1	AF033407	AF033407 Myxococcu
16	38.6	3.4	811	9	HSA343316	AJ343316 Homo sapi
17	38.4	3.4	1748	10	BC021429	BC021429 Mus muscu
18	38	3.3	157653	2	AC009033	AC009033 Homo sapi
19	38	3.3	205044	2	AC009125	AC009125 Homo sapi
20	37.6	3.3	204618	10	AF146793	AF146793 Mus muscu
21	37.4	3.3	140524	2	AP004660	AP004660 Oryza sat
22	37.2	3.3	176379	2	AC060833	AC060833 Homo sapi
23	36.4	3.2	17006	3	AF177871	AF177871 Drosophill
24	36.4	3.2	77409	3	AC004248	AC004248 Drosophill
25	36.4	3.2	98401	8	ATF27B13	ALU050352 Arabidops
26	36.4	3.2	111336	2	AC018305	AC018305 Drosophill
27	36.4	3.2	160827	3	AC099025	AC099025 Drosophill
28	36.4	3.2	161742	2	AC068100	AC068100 Homo sapi
29	36.4	3.2	167966	2	AC106774	AC106774 Homo sapi
30	36.4	3.2	168360	2	AC041048	AC041048 Homo sapi
31	36.4	3.2	169877	3	AC104612	AC104612 Drosophill
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33	36.4	3.2	262173	3	AE003808	AE003808 Drosophill
34	36.2	3.2	125020	9	AF429315	AF429315 Homo sapi
35	36.2	3.2	174927	2	AL445427	AL445427 Homo sapi
36	36.2	3.2	184743	9	AF003627	AF003627 Homo sapi
37	36.2	3.2	185799	30	AL390238	AL390238 Human DNA
38	36.2	3.2	188357	9	AL159996	AL159996 Human DNA
39	36.2	3.2	189760	9	AC093155	AC093155 Homo sapi
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41	36	3.2	1090	11	G54521	G54521 Xg3559 KMOK
42	36	3.2	128117	9	AC004000	AC004000 Human PAC
43	36	3.2	132581	2	AP003742	AP003742 Oryza sat
44	36	3.2	135038	9	HUMWMD703	L78810 Homo saplen
45	36	3.2	142707	2	AP004338	AP004338 Oryza sat

ALIGNMENTS

RESULT 1	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM
AF172445	AF172445	Plasmodium falciparum chitinase gene, complete cds.	AF172445	1	GI:5661403		Plasmodium falciparum

REFERENCE	AUTHORS	TITLE
1 (bases 1 to 1137)	Vinetz,J.M., Dave,S.K., Specht,C.A., Brameid,R.A., Xu,B., Hayward,R. and Fidock,D.A.	The chitinase pfCHN1 from the human malaria parasite Plasmodium falciparum lacks proenzyme and chitin-binding domains and displays unique substrate preferences

JOURNAL MEDLINE 20040676

REFERENCE 2 (bases 1 to 1137)

AUTHORS Vinetz,J.M. and Dave,S.K.

TITLE Direct Submission
Submitted (26-JUL-1999) Center for Tropical Diseases, University of Texas Medical Branch, 301 University Blvd., Galveston, TX

77555-0609, USA
Location/Qualifiers
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/chromosome="12"
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SCIGFNDPKIKCMDEAPYNSKYENKPDVKEKELIRAAQMSAGCAIYLMNLIKMDIM
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BASE COUNT 321 a 263 c 257 g 296 t
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Best Local Similarity 100.0%; Pred. No. 7, 1e-301;
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QY 61 actaagtctctgtatcgaagatcatcgctgctcggttgatcccgcaaaacccg 120
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QY 781 ggtgtgtccatctactcgtatgaagaacactgaaatatgatgacatggtgttgcgag 840
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QY 1021 actgaanaacactgaataaagcgcagatggttcggtcgtgctgctcgtccagcgac 1080
DB 1021 ACTGAANAACAACTGAATTAAGGCGCAGATGTTTCGCGCTGCTGCTGCTGCTGCTGCTG 1080
QY 1081 aacgcgcacataatgaacagctggtgacatgactcgttgaagaactgacata 1137
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LOCUS Plasmodium falciparum chromosome 12 clone 3D7, *** SEQUENCING IN
DEFINITION PROGRESS ***, 5 unordered pieces.
AC006279
AC006279.8 GI:9797723
HTG: HTGS_PHASE1.
KEYWORDS malaria parasite P. falciparum.
SOURCE Plasmodium falciparum
ORGANISM Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
REFERENCE 1 (bases 1 to 245802)
Hyman, R.W., Fung, E.L., Qin, F., Rowley, D., Mao, J., Tamaki, T.,
Kurd, O.B., Conway, A.B. and Davis, R.W.
Plasmodium falciparum 3D7 chromosome 12
Unpublished
JOURNAL Direct Submission
REFERENCE Hyman, R.W., Fung, E.L., Qin, F., Tamaki, T., Kurd, O.B. and Davis, R.W.
TITLE Submitted (05-JAN-1999) Stanford DNA Sequencing and Technology
AUTHORS Center, Stanford University, 855 California Avenue, Palo Alto, CA
JOURNAL 94304, USA
COMMENT
On Aug 12, 2000 this sequence version replaced gi:18810451.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 5 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 147568: contig of 147568 bp in length
* 147569 147768: gap of unknown length
* 147769 217470: contig of 69702 bp in length
* 217471 217670: gap of unknown length
* 217671 219372: contig of 1702 bp in length
* 219373 219572: gap of unknown length
* 219573 221333: contig of 1761 bp in length
* 221334 221533: gap of unknown length

QY 154 aaagatatacacaagggtactactccgtccgtgggtgagctataacacacctaagagac 213
AF216703 1 AAAGGAATTTATTCAGGTTATTCATCATGGGTTTCTTATTAATCATAACTTGAAAGAT 60
QY 214 ctgaaccggaacctgaacgctggtacacatgaagcttgcctaaatgaatgaatgaacgac 273
Db 61 TTAATGCTTAATTAATGTTGTAACATATGCTTTGCTAAGATGATGATTTCTATGAC 120
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RESULT 4
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LOCUS AF216703

DEFINITION Synthetic construct chitinase CHT1 (Chl1) gene, complete cds.
ACCESSION AF216703
VERSION AF216703.1 GI:8705223
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
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BASE COUNT 545 a 422 c 386 g 411 t
ORIGIN

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Best Local Similarity 52.28; Pred. No. 5; 6e-36;
Matches 512; Conservative 0; Mismatches 444; Indels 24; Gaps 5;

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Db 384 TCCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 443
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QY 339 tctgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaat 398
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Db 1192 GGGCAGCAGCATGTATACACAGAACTTTATTAATTTTATATACAGCAAGAGA 1251
QY 818 tgatgacatggtgttctgtagacgyltcaactcaacgaacttaccgttaccgtt 877
Db 1252 AAAATGATCTTGTATTTATTTCAACATACAAATTT--TAGAAATCTACAAATCCAGATATTA 1308
QY 878 tgaagaattatacgaactcctacgatactatggtataaagtagatcagatcatca 937
Db 1309 TGGTAGATATGCTACTTATCCATTTATTTGTTTAAATATATACATCAATCATAT 1368
QY 938 tgggtcaccctgagtlctccgcgtccagcgttcaaccgcaagataaagtctgttaa 997
Db 1369 TAGGTTTTCATTTAGAACATTAACAGAGGTGATTTAGTCCGAAATTAAGATATTTAG 1428
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Db 1429 AATTGGTAGGAAACATACATGATTAATAATCAAAATATATATAGGCGAGTGTATAG 1488
QY 1058 ggcctgtgctctgt 1072
Db 1489 GGAATATGCAATTTAT 1503

RESULT 6
PBE305256 2562 bp mRNA linear INV 30-MAY-2001
LOCUS Plasmodium berghel mRNA for chitinase (chl gene).
DEFINITION AJ305256
ACCESSION AJ305256 GI:14275848
VERSION AJ305256.1 GI:14275848
KEYWORDS chitinase; Chl1 gene.
SOURCE Plasmodium berghel.
ORGANISM Plasmodium berghel
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
REFERENCE 1 (bases 1 to 2562)
AUTHORS Dessens, J.T., Mendoza, J., Claudianos, C., Vinetz, J.M., Khater, E.,
Hassard, S., Ranawaka, G.R. and Sindén, R.E.
TITLE Knockout of the rodent malaria parasite chitinase pbchl1 reduces
infectivity to mosquitoes
JOURNAL Infect. Immun. 69 (6), 4041-4047 (2001)
REFERENCE 2 (bases 1 to 2562)
AUTHORS Dessens, J.T.
TITLE Direct Submision
JOURNAL Submitted (31-JAN-2001) Dessens J.T., Dept. of Biology, Imperial
College of Science, Technology and Medicine, SAFB, Imperial College
Road, London, SW7 2AZ, UNITED KINGDOM

FEATURES
source location/Qualifiers
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/strain="ANKA"
/isolate="2.34"
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/gene="chl1"
174..2120
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EYKRRKQGIAGYGSWNSOGASGKQMTSHNPVSLIYIAFAINNNYASRKYNEL
OKFLQKRGHLEPEETGMANEIKIRKARPDVLIISLGETVMIDITKEIDYPOIV
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ALSCVSWETFECDDEFPYNTQYLSQOMIVNPELYKASTMLSTGTFNVNFTAKDKID
LYFIQYVLETSPMDIMDMLYLHLKFGKDYITVPLGFSIEDNGRGSFSDSKRYVL
VSKAIDNNHNEFRADGVGIMHLPKQKMGATIDGFTIDNTWTHLNFKISKSTDI
SLPNPDGCSITIEEYVGVIPVGTYAKHNDALWVRSYSTRAFGIDRYEMNVLKQVY
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gene 174..2120
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mat_peptide 228..2117
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BASE COUNT 1001 a 323 c 416 g 822 t
ORIGIN

Query Match 6.2% Score 70.2; DB 3; Length 2562;
Best Local Similarity 45.4% Pred. No. 3.8e-08;
Matches 467; Conservative 0; Mismatches 538; Indels 24; Gaps 5;

QY 110 gcaaaacccgcggaatatacaaacgtttaagaatccggtaaagatcatccag 169
Db 631 GAAATCTCCAAAGGAAATTTTAAAGAAATATATAAAGAAAGCAAGATATATTCAG 630
QY 170 gtaactacgctcctggtgtagactataatcacacccgaaagaccty-----aac 220
Db 691 GATATTATGATCATGGAATAGCCAGAGAGCTACGGGAAACAAATGATCATTCACACC 750
QY 221 cgaacctgaacgtggttaccatgagcttctgtaaatgagattaaagtaactcatt 280
Db 751 CACAGTATCTATATATTTATATACCTTCGCCGTATTAATATGATATATGATCTTCTA 810
QY 281 aatccatgtagtagcccgctgctgtttaaacgctgattgacctgagatataatgctc 340
Db 811 AACCATATATGCACTTCAAAATTTTACAAAAGCAATGCACTGATTTGAAACAT 870
QY 341 tgaatgacttcaatgataatgataatgataatgataatgataatgataatgataatg 400
Db 871 ATGATATGATGCTAATGAAATTAAGCTATTAAGAAAGCCGCCGATGATATATAA 930
QY 401 tgcgagcctggtggtgagagacacacacacacacacacacacacacacacacacac 460
Db 931 TTTATATCTATGAGGAGGAAACATATC--ATGATATATATTAACAAAGAAATGATATA 987
QY 461 ttgaaataatgcgaactcgtgtgtagtaactggtcgtgtagttagttagttagttagt 520
Db 988 TTCTCAATATGTAACATGATGTTAACAATTTTGAATTTGATGATGATGATGATGATG 1047
QY 521 aaccgaacgagcgtttagttagttagttagttagttagttagttagttagttagttag 580
Db 1048 AACCAATGGAAGATTTTACATTTAATGAAAGCTTTCATTAATTTATTAATTAAT 1107
QY 581 acgtgacaaactcgtggaataatgtagttagttagttagttagttagttagttagttag 640
Db 1108 TGATTTGATTTTATTAAGAACCAATTTCTTAAGATTAAGCTAATTTCCATATCTGATCAT 1167
QY 641 ctaatgagcctcgtgagctgtagcgttcaacgacccgaaataatcgtatgtagttag 700
Db 1168 CAATTCAGCATTTATCAT-----GTGTATCATGATGAGACATTTTGTAAAGATGAAG 1221
QY 701 aagctcgtataacagaataatatt---caacaaaccggaacgttaagaagaacgtttag 757
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QY 818 tgatgacatggtgttctgtagacgyltcaactcaacgaacttaccgttaccgtt 877
Db 1342 AAAATGATCTTGTATTTATTTCAACATATATATTTAGAAACATTAACCCAGATTA---TCA 1398
QY 878 tgaagaattatacgaactcctacgatactatggtataaagtagatcagatcatca 937
Db 1399 TGGTAGATATGCTACTTATCCATTTATTTGTTTAAATATATACATCAATCATAT 1458
QY 938 tgggtcaccctgagtlctccgcgtccagcgttcaaccgcaagataaagtctgttaa 997
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QY	998	aatcatatcgggcatttcgttaaaaactgtaaaacaaactgaataaagcgcagatggttcg	1057
DB	1519	AATTAGTATCGAAGAACTATACATGACAAATAATACAGCAATTCATCAAGAGCGCGTGGTAG	1578
QY	1058	gacctggtcctctgcccagcgaacacgcggcccaatgaatgaacagctcgcgatcagttact	1117
DB	1579	GAATTGGCATTTATTATTATGGAAGAACAATGCTTAATGAGCATATGATCTAGATGGTT	1638
QY	1118	tcgttgaaa	1126
DB	1639	TTATTGATA	1647
RESULT	7		
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LOCUS	AX083744	1141 bp	DNA
DEFINITION	Sequence 22 from Patent WO0111061.		linear
ACCESSION	AX083744		
VERSION	AX083744.1	GI:13185472	
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS	Kunst,L. and Clemens,S.		
TITLE	Regulation of embryonic transcription in plants		
JOURNAL	Patent: WO 011061-A 22 15-FEB-2001;		
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promoter	/db_xref="taxon:32630"		
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BASE COUNT	123 a	32 c	42 g
ORIGIN			112 t 832 others
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Best Local, Similarity		10.1%	Pred. No. 0.63;
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QY	63	ttaatttcctgtacggaagtcacgcgcgtcgtccgttcggtatcccgaaacccgcg	122
DB	82	WTKKWTACANNTSBRYARRKKWDKKTAYBMTTKKKGCTGRHRYMKRRABDTVDHHY	141
QY	123	tgaattatcaaaacggtttaaagaatccggtaaagatatacatccaggtttactatccgtc	182
DB	142	VTAMNNATTTTCOMDXDKDKRTIRMMWKKKNNNNATGMDDTIKYHHMNNNGCBTYWMMRYKTD	201
QY	183	ctgggtgcgtataatcaacaacctgaagaacccaacccaacccaacccaacccaacccaac	242
DB	202	RDMSEKRNNGYGBMWMKNSYDVTYYWVWWDMDCKRKYRVWRTGRMRMYUWAMBTANRR	261
QY	243	gagcttgcctaataaggtttaagctacgactccaatgaatccalcscagctagtagccgcct	302
DB	262	RYNNCWTDAMAYRRRTMNNNNNNNAKAMKRRKAYGWMNRBVNSTTTMKSKTKTKYRTSCW	321
QY	303	gctgtttaaagccgtat-ttgcctctgagatataatgttctgaatgaatgaatgaatgaat	360
DB	322	ANNCBAGDANDDKMKWKSALMGVYUWNNNNNNNNMMTYKKARHBAARDWVHSMKKMHANA	381
QY	361	gccatgaatctcgcgcaaacgctcgcgcgaacattatagctgcgtgcgaaccccgcggtgag	420
DB	382	AHYSRKKMTBYXRRKTMVNNNGTTMKRMMWAMYMDMDWBDGTNNNNNGGRTYYGWTKN	441
QY	421	acctcaactcgctcctcctcgtatctgcactccaacgcggttgtaaaaatccgcaaatgc	480
DB	442	KKMPTYUWKANNCWRRAMDHKTCTHHNNTTWKKMTTYNNNNCTYMKSTYNGKSHRBAAYTT	501
QY	481	gtgagtagaactggccttcgatgtatgtatgtatgaatcaagaacccaacgcgacgtttgat	540

Dd		502	WTMMWRRAAHANNNNWIDWKACWIKYBYCVSKMWNNTAAWYTSSMNWTSRIIRKMTN	561
Oy		541	ggtctgaatgataagaanaagcgacttcttgtacatacgttgacaacatgcgcga	600
Dd		562	NSMHRSDPTBSRGRANNYARABHYGYKNWTRMBWSHVBHBRCAGAAHYWBMVBAKH	621
Oy		601	tacatgtgtgatgataaacatgcatcacatccagtcctctaattgcgccttgatgc	660
Dd		622	CMKARYKAKKYAGCGSNUNNNNNNNNNNNNNATCABDDYYAASRWYAMANAKEYKB	681
Oy		661	atcggtttcaaggaccggaaaaatctgtatgtagtcgaagcccgtlataacagcaa	720
Dd		662	AANNAYTHANNMWCGMNNAIDTTRTKMKNNNNNAGTWKNNNNNAKNAKAYAAA	741
Oy		721	-tatatacaacaacgcgactgtaagaagaactgtacgcgcagccagatgcatcgy	778
Dd		742	VKAARKHMRWAKMARMRGHADAAABTTDKRNAGAYTYTTNNNNNTYRGVYTNFAADG	801
Oy		779	cgggtgtgtgccatctacctgatalgaacaacatgaaatatgattgacatgltgtgtgc	838
Dd		802	WANNNNNNNNNNNNGSDMWVTWWAANYGTNNNNNNNNNAAWWTNKWYTTDDR	861
Oy		839	agacgttcaactacacgcgaacttaccgattctaccgattatga	880
Dd		862	RBAYTNNNNNNEMAYGAYADDYAYMSDTCDAWMKWATKM	903
RESULT		8		
ABO22908				
LOCUS	ABO22908	1624 bp	mRNA	linear INV 18-NOV-1999
DEFINITION	Apis mellifera mRNA for amylase, complete cds.			
ACCESSION	ABO22908			
VERSION	ABO22908.1 GI:6448462			
KEYWORDS	amylase.			
SOURCE	Apis mellifera adult female hypopharyngeal gland cDNA to mRNA.			
ORGANISM	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea; Apidae; Apsis.			
REFERENCE	Ohashi,K., Natori,S. and Kubo,T. Expression of amylase and glucose oxidase in the hypopharyngeal gland with an age-dependent role change of the worker honeybee Eur. J. Biochem. 265 (1), 127-133 (1999)			
AUTHORS	Ohashi,K., Natori,S. and Kubo,T.			
TITLE	2 (bases 1 to 1624) Direct Submission Submitted (27-JAN-1999) Kazuaki Ohashi, University of Tokyo, Faculty of Pharmaceutical Sciences, Hongo 7-3-1, Bunkyo-ku, Tokyo 113-0033, Japan (E-mail:kazuaki@mol.f.u-tokyo.ac.jp, Tel:81-3-3812-2111(ex.4823), Fax:81-3-5684-2973)			
JOURNAL	Location/Qualifiers			
MEDLINE	1. .1624			
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AUTHORS	/db_xref="taxon:7460"			
TITLE	/sex="female"			
JOURNAL	/tissue_type="hypopharyngeal gland"			
FEATURES	/dev_stage="adult"			
source	11. .1492			
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BASE COUNT      466 a      356 c      413 g      389 t
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Query Match      3.88; Score 43.6; DB 3; Length 1624;
Best Local Similarity 49.68; Pred. No. 0.74;
Matches 112; Conservative 0; Mismatches 114; Indels 0; Gaps 0;

Qy 858 ctctacgattctacgcttgaagaattatacagaccctcagcatctatgtaaaaa 917
Db 901 CTGAGAGATTCTCTCTTTTCGTGACATACGACACGCGACGCGACATCCCAAT 960
Qy 918 gtacgatacgtatcatcatalgagcttcacccgtatgtccgctcagccgttaacc 977
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Qy 978 gaacgataaaatcgtgtaaaatctatcgtcgtatcgttaaaaaactgaaactgaa 1037
Db 1021 ATTGCGTACCCCAAGATTAATGAGTTCTTCTGACTCCCAAGATCAAGGACCGCC 1080
Qy 1038 taaacgacgagatggttcgctgtgtctgtcctcagcgacaac 1083
Db 1081 TAATGACGCAATGCAACATTTCTGCGCTTGATCCAGCAAC 1126

RESULT 9
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LOCUS
DEFINITION      Sequence 22 from Patent WO0111061.
ACCESSION      AX083744
VERSION      AX083744.1 GI:13185472
KEYWORDS
SOURCE      synthetic construct.
ORGANISM      artificial sequence.
REFERENCE      1 (bases 1 to 1141)
AUTHORS      Kunst, L. and Clemens, S.
TITLE      Regulation of embryonic transcription in plants
JOURNAL      Patent: WO 011061-A 22 15-FEB-2001;
UNIVERSITY OF BRITISH COLUMBIA (CA)
FEATURES
source
1. 1141
/organism="synthetic construct"
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/promoter="consensus sequence of A.t., L.a., and B.n. FAEI
promoter
1. 1141
/note="consensus sequence of A.t., L.a., and B.n. FAEI
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Best Local Similarity 9.28; Pred. No. 2.2;
Matches 47; Conservative 216; Mismatches 247; Indels 0; Gaps 0;

Qy 566 actctcttgatgaacactgacccaactgacgacataatgtgatataaactgatca 625
Db 632 RMTMTMTMTMGDGTAVKAKKMRDTCTTYDVADSWWYANMMRCHDYTYTNNYCK 573
Qy 626 gcatcagcagctccctaatgagctcgtcgtcgtcgtcgttcaacgacccgaaaaa 685
Db 572 SYAHSYWYMNANMWRBYRYSARNSSMARWTTNNMMWSGBVRMRWAGTMWRHNNNT 513
Qy 686 tctgtatgtagcagaaccccgatataacgaaatattcaacaacccgagcttaaga 745
Db 512 DTRYWMMKRWABTTTVYSMCAKSMWRGNRRAMKMMWAAANNADGAMDHWTYMGNN 453
Qy 746 aagaactgtacgacgacccaagatgcatcgtcggtgtgcatcactatgtagaca 805
Db 452 TMMRRRWKMMNNAWCKRAACCCNNNNNRACVHKKMKMRWTWKYMKRACCCNNNNBKAMY 393
Qy 806 acctgaagaatgatgatgatgtgtgtgtgcagacgttcaactacgaaactctacg 865

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Db 392 RVAMMMYSRDTTNDMMMTSDMBMHMTYDTYTMRRAMNNNNNNNNNNBXCITTSMMMDH 333
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Db 332 MNTHTTNNNTGSAHYBMAASMMWAGASNBVTTNCKCRRTYTMCKTYTNNNNNNKMYTR 273
Qy 926 acglatcatatggtctcaccctgatgtctccgtcagccgcttcaaccgacgata 985
Db 272 TKTYAMCNRNRYDPAWTBKRNYKCYAABWYBYMKGKHMMWRMRABHRSMMNMMWYK 213
Qy 986 aatgctgttaaatctatcgtcgtcgttctgtaaaactgaaacaaactgaaacgag 1045
Db 212 CRNKYVMSWHYAMRYKMBAYVGCNNNNMKDRAHHHMCATNNNNMMWYAYHHHKKG 153
Qy 1046 cagatggttcgctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1075
Db 152 KAAMTNNKTABRDBAHVKTWYWRDYW 123

RESULT 10
AL359267/c      119526 bp      DNA      linear      PRI 16-NOV-2001
LOCUS
DEFINITION      Human DNA sequence from clone RP11-384P3 on chromosome 10, complete
ACCESSION      AL359267
VERSION      AL359267.37 GI:16973855
KEYWORDS      HMG.
SOURCE      human.
ORGANISM      Homo sapiens
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 119526)
AUTHORS      Blakey, S.
TITLE      Direct Submission
JOURNAL      Submitted (16-NOV-2001) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquerry@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk
On Nov 17, 2001 this sequence version replaced gi:16944914.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em: EMBL, Sw:
SWISSPROT, Tr: TrEMBL, Wp: WormPeP; Information on the WormPeP
database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone configs of human
chromosome 10, constructed by the Sanger Centre Chromosome 10
Mapping Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr10
RP11-384P3 is from the library RPCT-11.2 constructed by the group
of Pieter de Jong. For further details see
http://www.chori.org/Bacpac/home.htm
VECTOR: pBAC3.6
IMPORTANT: This sequence is not the entire insert of clone
RP11-384P3. It may be shorter because we sequence overlapping
sections only once, except for a short overlap.
The true left end of clone RP11-384P3 is at 1 in this sequence.
The true left end of clone RP11-166B18 is at 117527 in this sequence.
The true right end of clone RP11-96C4 is at 18855 in this sequence.
FEATURES
source
1. 119526
Location/Qualifiers

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Center: Whitehead Institute/ MIT Center for Genome Research
Center code: MIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L4823
Center clone name: 29_E_20
----- Summary Statistics
Sequencing vector: M13: M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 148808 bases at least Q40
Consensus quality: 153763 bases at least Q30
Consensus quality: 155236 bases at least Q20
Insert size: 170000; agarose-fp
Insert size: 156515; sum-of-contigs
Quality coverage: 4.1 in Q20 bases; agarose-fp
Quality coverage: 4.5 in Q20 bases; sum-of-contigs
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 21 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 1020: contig of 1020 bp in length
* 1021 1120: gap of 100 bp
* 1121 2314: contig of 1194 bp in length
* 2315 2414: gap of 100 bp
* 2415 2871: contig of 457 bp in length
* 2872 2971: gap of 100 bp
* 2972 5093: contig of 2122 bp in length
* 5094 5193: gap of 100 bp
* 5194 6740: contig of 1547 bp in length
* 6741 6840: gap of 100 bp
* 6841 10535: contig of 3655 bp in length
* 10536 10635: gap of 100 bp
* 10636 14161: contig of 3526 bp in length
* 14162 14261: gap of 100 bp
* 14262 18606: contig of 4345 bp in length
* 18607 18706: gap of 100 bp
* 18707 25158: contig of 6452 bp in length
* 25159 25258: gap of 100 bp
* 25259 31210: contig of 5952 bp in length
* 31211 31310: gap of 100 bp
* 31311 37297: contig of 5967 bp in length
* 37298 37397: gap of 100 bp
* 37398 44148: contig of 6751 bp in length
* 44149 44248: gap of 100 bp
* 44249 49736: contig of 5488 bp in length
* 49737 49836: gap of 100 bp
* 49837 59810: contig of 9974 bp in length
* 59811 59910: gap of 100 bp
* 59911 68630: contig of 8720 bp in length
* 68631 68730: gap of 100 bp
* 68731 78807: contig of 10077 bp in length
* 78808 78907: gap of 100 bp
* 78908 88451: contig of 9544 bp in length
* 88452 88551: gap of 100 bp
* 88552 98431: contig of 9880 bp in length
* 98432 98531: gap of 100 bp
* 98532 111619: contig of 13088 bp in length
* 111620 111719: gap of 100 bp
* 111720 126345: contig of 14626 bp in length
* 126346 126445: gap of 100 bp
* 126446 158515: contig of 32070 bp in length.
Location/Qualifiers
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RESULT 13
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LOCUS AC098565/c
DEFINITION Oryza sativa chromosome 10 clone OSJNBa0028C16, complete sequence.
ACCESSION AC098565
VERSION AC098565.3 GI:18056687
KEYWORDS HTG.
SOURCE Oryza sativa.
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzoae; Oryza.
REFERENCE
AUTHORS Wang, R.A., Yu, Y., Soderlund, C., Chen, M., Kim, H.-R., Rambo, T.,
Sasaki, C., Henry, D., Oates, R. and Simmons, J.
Rice Genomic Sequence
Unpublished
2 (bases 1 to 166757)
Wing, R.A., Yu, Y., Soderlund, C., Chen, M., Kim, H.-R., Rambo, T.,
Sasaki, C., Henry, D., Oates, R. and Simmons, J.
Direct Submission
Submitted (24-OCT-2001) Clemson University Genomics Institute,
Clemson University, 100 Jordan Hall, Clemson, SC 29634, USA
3 (bases 1 to 166757)
Wing, R.A., Yu, Y., Soderlund, C., Chen, M., Kim, H.-R., Rambo, T.,
Sasaki, C., Henry, D., Oates, R. and Simmons, J.
Direct Submission
Submitted (12-NOV-2001) Clemson University Genomics Institute,
Clemson University, 100 Jordan Hall, Clemson, SC 29634, USA
4 (bases 1 to 166757)
Wing, R.A., Yu, Y., Soderlund, C., Chen, M., Kim, H.-R., Rambo, T.,
Sasaki, C., Henry, D., Oates, R., Simmons, J., Thurmond, S.K. and Sun, S.
Direct Submission
Submitted (22-NOV-2001) Clemson University Genomics Institute,
Clemson University, 100 Jordan Hall, Clemson, SC 29634, USA
5 (bases 1 to 166757)
Wing, R.A., Yu, Y., Soderlund, C., Chen, M., Kim, H.-R., Rambo, T.,
Sasaki, C., Henry, D., Oates, R. and Simmons, J.
Direct Submission
Submitted (04-JAN-2002) Clemson University Genomics Institute,
Clemson University, 100 Jordan Hall, Clemson, SC 29634, USA
6 (bases 1 to 166757)
Wing, R.A., Yu, Y., Soderlund, C., Chen, M., Kim, H., Rambo, T.,
Sasaki, C., Henry, D., Oates, R., Simmons, J., Thurmond, S.K. and Sun, S.
Direct Submission
Submitted (30-JAN-2002) Clemson University Genomics Institute,
Clemson University, 100 Jordan Hall, Clemson, SC 29634, USA
7 (bases 1 to 166757)
Wing, R.A., Yu, Y., Soderlund, C., Chen, M., Kim, H., Rambo, T.,
Sasaki, C., Henry, D., Oates, R., Simmons, J., Thurmond, S.K. and Sun, S.
Direct Submission
Submitted (03-FEB-2002) Clemson University Genomics Institute,
Clemson University, 100 Jordan Hall, Clemson, SC 29634, USA
On Jan 4, 2002 this sequence version replaced gi:16904378.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred
quality>=30); an attempt was made to resolve all sequencing
problems, such as compressions and repeats; all regions were
covered by more than one plasmid subclone; and the assembly was
confirmed by restriction digest. From base 102398-102518 there is
some low quality. Bacterial transposons span the areas located at
26317-28840 and 67280-69982. The assembly overlaps from base
1-15763 with OSJNBa0031A07 (accession #AC084884). The overlap is
from bases 118791-134553 of OSJNBa0031A07.

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 7, 2002, 11:49:39 ; Search time 247.46 Seconds
(without alignments)
7888.676 Million cell updates/sec

Title: US-09-579-383-1

Perfect score: 1137
Sequence: 1 atgaatttaccgtaataa.....tcgttgaaagctgcactaa 1137

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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24: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1137	100.0	1137	22 AAC89668	P. falciparum chit
2	104.2	9.2	1764	22 AAC89669	P. gallinaceum chl
3	104.2	9.2	2500	22 AAC89670	P. gallinaceum chl
4	38	3.3	4590	22 AAH24065	Yeast AOD9604-asso
C	36.4	3.2	2258	23 ABLO9857	Drosophila melanog
C	36.4	3.2	4553	23 ABLO9856	Drosophila melanog
C	36.4	3.2	6488	23 ABLO302	Drosophila melanog
7	35.2	3.1	3294	23 AAS73382	DNA encoding novel
9	35.2	3.1	3294	23 AAS89403	DNA encoding novel

C	10	35.2	3.1	3294	23 AAS94292	DNA encoding novel
C	11	35.2	3.1	3296	23 AAS92034	DNA encoding novel
C	12	34.8	3.1	2111	19 AAB14467	H. pylori GPO 103
C	13	34.8	3.1	2307	23 ABL23687	Drosophila melanog
C	14	34.8	3.1	5479	23 ABL23686	Drosophila melanog
C	15	34.8	3.1	27425	21 AAS53978	DMP53 tumour suppr
C	16	34.6	3.0	4729	11 AAQ04043	Recombinant DNA fo
C	17	34.4	3.0	42000	21 AAB63349	Streptomyces globi
C	18	34.4	3.0	63164	21 AAB63348	Streptomyces globi
C	19	34.4	3.0	3172	22 AAS34789	CDNA encoding nove
C	20	34	3.0	3202	18 AAT47520	Human hepatoma-der
C	21	34	3.0	3256	22 AAS33262	DNA encoding human
C	22	34	3.0	3256	22 AAS34946	CDNA encoding nove
C	23	34	3.0	3316	19 AAV44859	Clone AQ7.3 codin
C	24	34	3.0	3316	22 AAF98456	Human cDNA clone A
C	25	34	3.0	3707	22 AAS34889	CDNA encoding nove
C	26	33.8	3.0	8196	23 ABL02886	Drosophila melanog
C	27	33.8	3.0	133894	17 AAT13635	ACNPV genomic DNA
C	28	33.8	3.0	1038602	20 AAT01425	Complete genome se
C	29	33.6	3.0	92407	22 AAF28549	Genomic fragment #
C	30	33.4	2.9	2100	23 ABL20941	Drosophila melanog
C	31	33.4	2.9	2149	18 AAT91115	Absidia blakesleea
C	32	33.4	2.9	2149	19 AAV59380	Nucleotide sequenc
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C	38	33.4	2.9	5040	21 AAB11351	Rice blast fungus-
C	39	33.4	2.9	22243	18 AAV74475	Staphylococcus aur
C	40	33.2	2.9	817	22 AAB07130	Human cDNA clone (
C	41	33.2	2.9	1148	22 AAB14736	Human cDNA sequenc
C	42	33.2	2.9	1177	21 AAC77080	Human OREF ORF2635
C	43	33.2	2.9	3102	22 AAB90796	CPE 100 coding seg
C	44	33	2.9	361	14 AAO59777	Human brain Expres
C	45	33	2.9	1539	23 AAS84960	DNA encoding novel

ALIGNMENTS

RESULT	1
ID	AAC89668 standard; DNA; 1137 BP.
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XX	AAC89668;
XX	
DT	13-MAR-2001 (first entry)
DE	P. falciparum chitinase coding sequence SEQ ID NO: 1.
DE	
KW	Malaria; mosquito; chitinase; fungal disease; parasitic disease;
KW	veterinary disease; arthropod pest; ds.
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OS	Plasmodium falciparum.
XX	
PN	MO200073488-A1.
XX	
PD	07-DEC-2000.
XX	
PF	26-MAY-2000; 2000MO-US14536.
XX	
PR	28-MAY-1999; 99US-0136508.
PR	03-FEB-2000; 2000US-0180051.
XX	
PA	(TEXA) UNIV TEXAS SYSTEM.
XX	
PI	Vinetz JM;
XX	
DR	WPI: 2001-061553/07.
DR	P-PSDB; AAB49985.
XX	
PT	New nucleic acid encoding a Plasmodium species chitinase is useful for

PT preventing transmission of malaria by mosquito feeding on subject that
PT may harbor Plasmodium species organisms -
XX
PS Claim 4; Page 123; 137pp; English.

XX The present invention provides the protein and coding sequences of the
CC Plasmodium falciparum and P. gallinaceum chitinase enzymes. These
CC organisms are the cause of malaria in humans. The sequences are useful
CC in the prevention and treatment of malaria, fungal diseases, parasitic
CC diseases and veterinary diseases, in preventing the transmission of
CC malaria and in the control of arthropod pests in agriculture.
XX

SQ Sequence 1137 BP; 321 A; 263 C; 257 G; 296 T; 0 other;

Query Match 100.0%; Score 1137; DB 22; Length 1137;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2

AAC89669
ID AAC89669 standard; DNA; 1764 BP.

XX AAC89669;

DT 13-MAR-2001 (first entry)

DE P. gallinaceum chitinase coding sequence SEQ ID NO: 2.

XX Malaria; mosquito; chitinase; fungal disease; parasitic disease;
KW veterinary disease; arthropod pest; ds.

OS Plasmodium gallinaceum.

PN MO200073488-A1.

XX 07-DEC-2000.

XX 26-MAY-2000; 2000WO-US14536.

PF 28-MAY-1999; 99US-0136508.

PR 03-FEB-2000; 2000US-0180051.

XX (TEXA) UNIV TEXAS SYSTEM.

PA Vlnetz JM;

XX WPI: 2001-061553/07.

DR P-PsDB: AAB49986.

XX New nucleic acid encoding a Plasmodium species chitinase is useful for
PT preventing transmission of malaria by mosquito feeding on subject that
PT may harbor Plasmodium species organisms -

XX Claim 4; Page 123-124; 137pp; English.

PS The present invention provides the protein and coding sequences of the
CC Plasmodium falciparum and P. gallinaceum chitinase enzymes. These
CC organisms are the cause of malaria in humans. The sequences are useful
CC in the prevention and treatment of malaria, fungal diseases, parasitic
CC diseases and veterinary diseases, in preventing the transmission of
CC malaria and in the control of arthropod pests in agriculture.
XX

SQ Sequence 1764 BP; 717 A; 227 C; 294 G; 526 T; 0 other;

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Matches 468; Conservative 0; Mismatches 483; Indels 24; Gaps 5;

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QY 170 gttactatccgcctgggtgagctataacac-----acctgaagcctcgaac 220
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QY 341 tgaatgagtaactactatgatgcatgaatctgacgaagctgctcgcgaatattatagc 400
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   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 917 ggcgcgcgcgcatgttatacagcagaaactttataattattttataacagcaagagata 976
QY 818 tgatgacatggtgttctgtagacggttcaactacacgaactctacgatttaccggtta 877
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 977 aaatgactctgtatttatttcaacatacaatt---tagaacctcaaatccagatata 1033
QY 878 tgaagaatatacagaccctcaacgatactatgtaaaaaaagtagatgaatgtagatcatca 937
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1034 tggtagatagatgtaacttccatttataatttgggtttaaataataacacacatacat 1093
QY 938 tgggcttacccctgtagtcccgctccacgcccgttcaaccgcggaagataaaatgctgataa 997
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1094 taggttttcaatttagaataataacagaggtgattagctccggaataaataagaattatag 1153
QY 998 aatcatcgcgatcttctgtaaaaaactgaanaacaaactgtaaaaaagcgacagatgtttc 1057
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1154 aattgtagtaaaaaaacaatacatatgataaaaatacaaaataaataatgagcgagatgtatag 1213
QY 1058 gccgtgtgtctctgt 1072
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1214 ggcataggcattat 1228

```

RESULT 3
AAC89670
ID AAC89670 standard: DNA: 2500 BP.

```

XX AAC89670:
AC 13-MAR-2001 (first entry)
DT
XX
XX
DE P. gallinaceum chitinase coding sequence SEQ ID NO: 5.
XX
XX
XX Malaria: mosquito; chitinase; fungal disease; parasitic disease;
KW veterinary disease; arthropod pest; ds.
XX
OS Plasmidium gallinaceum.
XX
XX WO200073488-A1.
XX
XX PD 07-DEC-2000.
XX
XX PF 26-MAY-2000; 2000MO-US14536.
XX
XX PK 28-MAY-1999; 99US-0136508.
XX
XX PR 03-FEB-2000; 2000US-0180051.
XX
XX (TEXA ) UNIV TEXAS SYSTEM.
XX
XX PA
XX PI Vinetz JM;
XX
XX DR WPI; 2001-061553/07.
XX
XX PT New nucleic acid encoding a Plasmidium species chitinase is useful for
XX preventing transmission of malaria by mosquito feeding on subject that
XX may harbor Plasmidium species organisms
XX
XX PS Disclosure; Page 127-128; 137pp; English.
XX
XX
CC The present invention provides the protein and coding sequences of the
CC Plasmidium falciparum and P. gallinaceum chitinase enzymes. These
CC organisms are the cause of malaria in humans. The sequences are useful
CC in the prevention and treatment of malaria, fungal diseases, parasitic
CC diseases and veterinary diseases, in preventing the transmission of
CC malaria and in the control of arthropod pests in agriculture.
XX
XX
SQ Sequence 2500 BP; 993 A; 283 C; 365 G; 858 T; 1 other;

Query Match 9.2%; Score 104.2; DB 22; Length 2500;
Best Local Similarity 48.0%; Pred. No. 1.4e-21;
Matches 468; Conservative 0; Mismatches 483; Indels 24; Gaps 5;

QY 110 gcaaaacccgcgtgaattatcaaaacglttaagaatcggtaagatcatccagg 169
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 541 gaaatcaccaagacaattttagaggagtaaaaaaagaaacaggtattatagcag 600
QY 170 gttactatccgcctgggtgagctataacac-----acctgaagcctcgaac 220
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 601 gatactatggttcaggaacagtcagtgatagagcaaaacatgattgattcaaac 660
QY 221 cgaacctgaacgtggttcacagatgacttgcctaaatgatttaagctacagctccatg 280
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 661 caatggtgtaaatattatataatgttcgtccgcatcaatattgttatatgtatccta 720
QY 281 aatccatcgtatgtagcccgctgctgtttaaagccctgattggtcctgagatattgtgc 340
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 721 gaccatttaatgagaacaaagatccctatttaagaanaacgcttaagataagaaact 780
QY 341 tgaatgagtaactactatgatgcatgaatctgacgaagctgctcgcgaatattatagc 400
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 781 atgatatgtagcttaataagaaattagacgatacagaanaagtaagtcacagatgtaattatc 840
QY 401 tgcctgagcctggcggtgtagacactacacacgctccctcctcctgactctgactcaacgcg 460
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 841 ttattactcttaggttggaagaaact--atatgatatgatatagaanaagaaattgattatg 897
QY 461 ttgaaaaaatcgcaaatctggtgtagaactggtcgtcgtgattgattgtagattagc 520
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

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Db 898 tgcataaataatgaagcttgtaattgattagatggtgtagatattgactg 957
QY 521 aaccgaacgagcgttctgattgctgtaataagaacgagactcttctacac 580
Db 958 aaccacatgggaatttaccacttaaatatttcaattatattatataat 1017
QY 581 acgtgacacactgcgacatcatggtgtgataaactgcagactcagccgct 640
Db 1018 taattactgtttaagaanaactcttcggaagaanaagtaattcattctgtt 1077
QY 641 ctaatgcgctctgagctgcatcggttcaacgaccgaaaaaactcgtatgtag 700
Db 1078 caatgctcattatcatcgcttccagagtgatgcac-----cttcgtaaagaag 1131
QY 701 aagctcgtataacagcaaatatt---caacaacgagcgttaagaagaagcgttac 757
Db 1132 aatcccatataaacaataaatttctgctgaacaataagaacaataagaattacata 1191
QY 758 gcgcagccagatgcatctgcggtggtgcacatcactgatacgaacctgaagata 817
Db 1192 gggcagcagcagtgattacagcaggaactttattatattttatatacagaagaga 1251
QY 818 tgattgacatggtgttctgacagcgttcaactacagaaactcagattaccgta 877
Db 1252 aatatagatctgtatttatttcaacatacaatt---tagaaactacaatccagatalaa 1308
QY 878 tgaagaattatacagactcctcagcatactatgttaaaaagtagattagcgtacata 937
Db 1309 tggtaagatgtaacttaccattatatttggtttaataatacatcacacaacatc 1368
QY 938 tgggcttcacccgtatgttccgcctccacgcgcttcaaccgagacataaatcgtgtaa 997
Db 1369 tagttttcttcatgaacataacagaggtgatttagtcccgaaataaagaattatag 1428
QY 998 aatctatcgcgagatttcgttaaaaactgaaaacaaactgaataagcgagatgttcg 1057
Db 1429 aattgtaagataaacaacatatacatataaatacaataataatagggcagatggtatag 1488
QY 1058 gccctgtgctcgt 1072
Db 1489 ggatagtgcatattat 1503

```

```

FT misc_feature 3819
FT /tag= e
FT /note= "Represented as * in the specification"
FT misc_feature 3862
FT /tag= f
FT /note= "Represented as * in the specification"
FT misc_feature 3864
FT /tag= g
FT /note= "Represented as * in the specification"
FT misc_feature 3888
FT /tag= h
FT /note= "Represented as * in the specification"
FT misc_feature 3890
FT /tag= i
FT /note= "Represented as * in the specification"
FT misc_feature 3912
FT /tag= j
FT /note= "Represented as * in the specification"
FT misc_feature 3914
FT /tag= k
FT /note= "Represented as * in the specification"
FT misc_feature 3938
FT /tag= l
FT /note= "Represented as * in the specification"
FT misc_feature 3939
FT /tag= m
FT /note= "Represented as * in the specification"
FT misc_feature 3941
FT /tag= o
FT /note= "Represented as * in the specification"
FT misc_feature 3943
FT /tag= p
FT /note= "Represented as * in the specification"
FT misc_feature 4361
FT /tag= q
FT /note= "Represented as * in the specification"

WO200133977-A1.
17-MAY-2001.
06-NOV-2000; 2000WO-AU01362.
05-NOV-1999; 99AU-0003875.
(META-) METABOLIC PHARM LTD.
Belyea CI, Ng FM, Vaughan P;
WPI; 2001-328876/34.

XX New organisms containing nucleic acid encoding a growth hormone
XX fragment which modulates lipid metabolism are useful to produce dietary
XX aids for obesity and in the meat production industry
XX
XX Disclosure; Page 48-50; 54pp; English.
XX
XX The invention relates to novel transgenic organisms useful in the
XX production of functional food and drink products for the treatment
XX or prevention of obesity via the regulation of lipid metabolism. The
XX organisms comprise a polynucleotide encoding a growth hormone fragment
XX capable of stimulating the activity of hormone-sensitive lipase (the key
XX enzyme in lipolysis) and inhibiting acetyl CoA carboxylase (the key
XX enzyme in lipogenesis). The growth hormone fragment preferably contains
XX at least the disulphide-bonded loop of a mammalian growth hormone (but is
XX not the full-length growth hormone) and is optionally linked to an
XX epitope tag or heterologous fusion protein partner. The transgenic
XX organism may be a microorganism used to produce a fermented product
XX (e.g., yeast), or an edible plant or animal or cell thereof. Food or
XX drink made using methods of the invention are used to modify fat/lean
XX ratio, lipid metabolism or food use in a mammal. In particular, the food
XX or drink products may be used to treat or prevent obesity, particularly
XX in humans, and may also be used to improve the fat/lean ration of

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XX Claim 1; SEQ ID NO 24050; 21pp + Sequence Listing; English.
PS
XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from *Drosophila*. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (AB101840-AB16175), expressed DNA
CC sequences (AB101840-AB16175) and the encoded proteins
CC (AB857737-AB872072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 4553 BP; 1404 A; 993 C; 901 G; 1255 T; 0 other;

Query Match 3.2%; Score 36.4; DB 23; Length 4553;
Best Local Similarity 51.2%; Pred. No. 2.5;
Matches 85; Conservative 0; Mismatches 81; Indels 0; Gaps 0;

OY 502 ggtatgtatgtatgattacgaacgacgacgacgttgatgtctgaatgataaagaaaa 561
DB 3150 GGAACCTCATGCTGATGCTTAGAGAACGTCATGCTGTTCTTGCTGTAAGTAATCA 3091
OY 562 gcggactctcttgatcaatacgtgacacactgcggaatacatgttgatgataaactg 621
DB 3090 ACAGATTTCGTTAACTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3031
OY 622 atcagcatcagccagctcctcctaactgagcgctgagctgacatcgatt 667
DB 3030 ATAAACATAGACTTTCTCAAACTTAACAACAATGCAATCGGCT 2985

RESULT 7
AB10302/c
ID AB10302 standard; cDNA; 6488 BP.
XX
XX AB10302;
AC
XX
XX 26-MAR-2002 (first entry)
DT
XX
XX *Drosophila melanogaster* expressed polynucleotide SEQ ID NO 25388.
DE
XX
XX *Drosophila*; developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ss.
XX
XX *Drosophila melanogaster*.
OS
XX
XX WO200171042-A2.
PN
XX
XX 27-SEP-2001.
PD
XX
XX 23-MAR-2001; 2001MO-US09231.
PF
XX
XX 23-MAR-2000; 2000US-191637P.
PR
XX
XX 11-JUL-2000; 2000US-0614150.
PR
XX
XX (PEKE) PE CORP NY.
PA
XX
XX Venter JC, Adams M, Li PMD, Myers EW;
PI
XX
XX WPI; 2001-656860/75.
DR
XX
XX P-PSDB; AB866199.
DR
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from *Drosophila* and for elucidating cell signalling and cell-cell
PT interactions -
XX
XX Claim 1; SEQ ID NO 25388; 21pp + Sequence Listing; English.
PS
XX
XX The invention relates to an isolated nucleic acid detection reagent

CC capable of detecting 1000 or more genes from *Drosophila*. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (AB101840-AB16175), expressed DNA
CC sequences (AB101840-AB16175) and the encoded proteins
CC (AB857737-AB872072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 6488 BP; 1991 A; 1324 C; 1311 G; 1862 T; 0 other;

Query Match 3.2%; Score 36.4; DB 23; Length 6488;
Best Local Similarity 51.2%; Pred. No. 3;
Matches 85; Conservative 0; Mismatches 81; Indels 0; Gaps 0;

OY 502 ggtatgtatgtatgattacgaacgacgacgacgttgatgtctgaatgataaagaaaa 561
DB 393 GGAACCTCATGCTGATGCTTAGAGAACGTCATGCTGTTCTTGCTGTAAGTAATCA 334
OY 562 gcggactctcttgatcaatacgtgacacactgcggaatacatgttgatgataaactg 621
DB 333 ACAGATTTCGTTAACTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 274
OY 622 atcagcatcagccagctcctcctaactgagcgctgagctgacatcgatt 667
DB 273 ATAAACATAGACTTTCTCAAACTTAACAACAATGCAATCGGCT 228

RESULT 8
AAS73382
ID AAS73382 standard; cDNA; 3294 BP.
XX
XX AAS73382;
AC
XX
XX 13-FEB-2002 (first entry)
DT
XX
XX DNA encoding novel human diagnostic protein #9186.
DE
XX
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200175067-A2.
PN
XX
XX 11-OCT-2001.
PD
XX
XX 30-MAR-2001; 2001MO-US08631.
PF
XX
XX 31-MAR-2000; 2000US-0540217.
PR
XX
XX 23-AUG-2000; 2000US-0649167.
PR
XX
XX (HYSE-) HYSEQ INC.
PA
XX
XX Drmanac RT, Liu C, Tang YT;
PI
XX
XX WPI; 2001-639362/73.
DR
XX
XX P-PSDB; AB609195.
DR
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
XX Claim 1; SEQ ID NO 9186; 103pp; English.
PS
XX
XX The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The

DR WPI; 2001-639362/73.
DR P-PSDB; ABG30105.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
PS Claim 1; SEQ ID No 30096; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pcl_sequences.
XX
SQ Sequence 3294 BP; 705 A; 943 C; 926 G; 720 T; 0 other;

Query Match 3.1%; Score 35.2; DB 23; Length 3294;
Best Local Similarity 52.0%; Pred. No. 4.9;
Matches 79; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

QY 549 tgataaagaagaacgagactcttctgtacaatacgtgacaaactgcgcgaatacatgtg 608
DB 1093 TGTATGGAATAACCATCTTCGATGGGACTTTGAGAACCACTTTTGTGCCGCTTAT 1034
QY 609 tgatgataaactgatacgaatcagccagtcctctaattgycgctctgagctgcatcggtt 668
DB 1033 TGCAGATTAACCGATCGCTTATGATGATGCAATAACGATTTGCCCTTCGTGACCT 974
QY 669 caacgacccgaaaaaactcgtatgtagtgcg 700
DB 973 CAACGAACAGTTGGATTAATATGTCGCTAATG 942

RESULT 11
AAS92034
ID AAS92034 standard; cDNA; 3296 BP.
XX
AC AAS92034;
XX
DT 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #27838.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensics;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN WO2001/5067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001MO-US08631.
XX

PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR P-PSDB; ABG27847.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
PS Claim 1; SEQ ID No 27838; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pcl_sequences.
XX
SQ Sequence 3296 BP; 720 A; 927 C; 940 G; 709 T; 0 other;

Query Match 3.1%; Score 35.2; DB 23; Length 3296;
Best Local Similarity 52.0%; Pred. No. 4.9;
Matches 79; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

QY 549 tgataaagaagaacgagactcttctgtacaatacgtgacaaactgcgcgaatacatgtg 608
DB 2202 tgatgataaactgatacgaatcagccagtcctctaattgycgctctgagctgcatcggtt 2261
QY 609 tgatgataaactgatacgaatcagccagtcctctaattgycgctctgagctgcatcggtt 668
DB 2262 tgcagataaaccgatacgcctcattgatacgcgaataaagaattgcccctcgtgacct 2321
QY 669 caacgacccgaaaaaactcgtatgtagtgcg 700
DB 2322 caacgacagttgataataatgctgctaattg 2353

RESULT 12
AAX14467/C
ID AAX14467 standard; DNA; 2111 BP.
XX
AC AAX14467;
XX
DT 31-MAR-1999 (first entry)
XX
DE H. pylori GHPO 1039 gene.
XX
KW GHPO protein; Helicobacter infection; gastroduodenal disease; gastritis;
KW peptic ulcer disease; ss.
XX
OS Helicobacter pylori.
XX

XX Key Location/Qualifiers
FH CDS 31..2070
FT /*tag= a
XX
XX MO9843478-A1.
XX
XX 08-OCT-1998.
XX
XX 01-APR-1998; 98WO-US06371.
XX
XX 29-JUL-1997; 97US-0902615.
PR 01-APR-1997; 97US-0833457.
PR 24-JUN-1997; 97US-0881227.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PA (IMMR) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS.
XX
XX Al-Garawi A, Kleanthous H, Miller C, Oomen RP, Tomb J;
XX
XX WPI: 1998-542293/46.
DR P-PSDB; AAM98748.
XX
XX
XX New isolated Helicobacter polynucleotides - used to develop products
PT for the diagnosis, prevention and treatment of Helicobacter
PT infections and gastrointestinal diseases
XX
XX Claim 1: Page 1597-1600; 2054pp; English.
XX
XX This sequence represents a polynucleotide of the invention. It was
CC isolated from Helicobacter pylori and encodes a H.pylori GHP0 protein.
CC The polypeptides can be used for preventing or treating Helicobacter
CC infections, and gastroduodenal diseases associated with these
CC infections, including acute, chronic, and atrophic gastritis, and peptic
CC ulcer diseases, e.g. gastric and duodenal ulcers. They can also be used
CC for the production of antibodies. The products can also be used for
CC detection and diagnosis.
XX
XX Sequence 2111 BP; 752 A; 392 C; 426 G; 541 T; 0 other;
XX
XX
XX Query Match 3.1%; Score 34.8; DB 19; Length 2111;
Best Local Similarity 58.8%; Pred. No. 5.1;
Matches 60; Conservative 0; Mismatches 42; Indels 0; Gaps 0;
XX
XX 236 ttcaatgagcttgcttaaatgatttaagctacgactccatcgaatcgcgtgagta 295
DB 1889 TTCAAAACATGATGGCCAAATGAGCTAAATCCACGACTTCCTGTAGCGCTTTGGCG 1830
XX
XX 296 gccgcgtgctgtttaaaagcctgattggcctgagatattg 337
DB 1829 TTATGCGTGTCTTTAAATGAGCTGCTTGGCTTTTGG 1788
XX
XX
XX RESULT 13
XX ABL23687
ID ABL23687 standard; DNA: 2307 BP.
XX
XX ABL23687;
XX
XX 26-MAR-2002 (first entry)
XX
XX Drosophila melanogaster genomic polynucleotide SEQ ID NO 22534.
XX
XX Drosophila; developmental biology; cell signalling; insecticide;
XX pharmaceutical; gene; ds.
XX
XX Drosophila melanogaster.
XX
XX WO200171042-A2.
XX
XX 27-SEP-2001.

PF 23-MAR-2001; 2001WO-US09231.
XX
XX 23-MAR-2000; 2000US-191637P.
PR 11-JUL-2000; 2000US-0614150.
XX
XX (PEKE) PE CORP NY.
XX
XX Venter JC, Adams M, Li PWD, Myers EW;
PI
PI WPI: 2001-656860/75.
XX
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX
XX
XX Claim 1; SEQ ID NO 22534; 21pp + Sequence Listing; English.
XX
XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (AB16176-AB130511), expressed DNA
CC sequences (AB101840-AB16175) and the encoded proteins
CC (AB57737-AB572072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pcl_sequences.
XX
XX Sequence 2307 BP; 524 A; 665 C; 647 G; 471 T; 0 other;
XX
XX
XX Query Match 3.1%; Score 34.8; DB 23; Length 2307;
Best Local Similarity 53.7%; Pred. No. 5.4;
Matches 72; Conservative 0; Mismatches 62; Indels 0; Gaps 0;
XX
XX 401 tgcgtagcctggcgggtgagactaccatcgctccctcctgattctgcactcaacgcgg 460
DB 611 tgcgtgagcagcaggacaaagaccgctccgagcgttcgctgcggtccatcacgagc 670
XX
XX 461 ttgaaaatacgcaactcgtggtgagtaactggttcgatgtattgataagattagc 520
DB 671 aggaatcatatgagacacagcagtgccacgaacggtccatgaaagtgcacactgttcctacg 730
XX
XX 521 aaccgaacgcagc 534
DB 731 agctgtacgcaac 744
XX
XX
XX RESULT 14
XX ABL23686/C
ID ABL23686 standard; DNA: 5479 BP.
XX
XX ABL23686;
XX
XX 26-MAR-2002 (first entry)
XX
XX Drosophila melanogaster genomic polynucleotide SEQ ID NO 22531.
XX
XX Drosophila; developmental biology; cell signalling; insecticide;
XX pharmaceutical; gene; ds.
XX
XX Drosophila melanogaster.
XX
XX WO200171042-A2.
XX
XX 27-SEP-2001.
XX
XX 23-MAR-2001; 2001WO-US09231.
XX
XX 23-MAR-2000; 2000US-191637P.
PR 11-JUL-2000; 2000US-0614150.
XX

PA (PEKE) PE CORP NY.
 XX
 PI Venter JC, Adams M, Li PMD, Myers EM;
 XX WPI; 2001-656860/75.
 DR
 XX
 PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -
 XX
 PS Claim 1: SEQ ID NO 22531; 21pp + Sequence Listing: English.
 XX
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (AB116176-AB130511), expressed DNA
 CC sequences (AB101840-AB116175) and the encoded proteins
 CC (AB187737-AB1872072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 CC
 SQ Sequence 5479 BP; 1370 A; 1352 C; 1353 G; 1404 T; 0 other;
 Query Match 3.1%; Score 34.8; DB 23; Length 5479;
 Best Local Similarity 53.7%; Pred. No. 8.6; Mismatches 62; Indels 0; Gaps 0;
 Matches 72; Conservative 0; Mismatches 62; Indels 0; Gaps 0;
 OY 401 tgcctgagcctggtgagacccatccgctccttcgattctgactcaacgcg 460
 DB 2971 TCGTAGCGACGACGAGACCGTCCGCGACGCTTTCGCGCGCTCCATACGACG 2912
 OY 461 ttgaaaaatcgcaatctgtgtgatacgtgcttcgattgattgattacg 520
 DB 2911 AGGAGTACATGAGAACCAATGCGACGAGCGGCGCATCGAAAGTACAACTGTTCTACG 2852
 OY 521 aaccgaacgcgcgc 534
 DB 2851 AGCTGTACGCCAAC 2838
 RESULT 15
 AAA53978
 ID AAA53978 standard; DNA; 27425 BP.
 AC AAA53978;
 XX
 DT 08-FEB-2001 (first entry)
 XX
 DE DMP53 tumour suppressor gene (genomic DNA).
 XX
 KW p53: tumour suppressor gene; insect; phenotype; metazoa;
 KW invertebrate; screening; pharmaceutical; pesticide; mis-expression;
 KW mutation; modulation; ds.
 XX
 OS Drosophila melanogaster.
 XX
 PN WO200055178-A1.
 PD 21-SEP-2000.
 XX
 PF 13-MAR-2000; 2000WO-US06602.
 XX
 PR 16-MAR-1999; 99US-0268969.
 PR 23-FEB-2000; 2000US-0184373.
 XX
 PA (EXEL-) EXELIXIS INC.
 XX
 PI Buchman AR, Platt DM, Olman MM, Young LM, Demsky MR, Keegan KP;
 PI Friedman L, Kopczynski C, Larson JS, Robertson SA;

XX
 DR WPI; 2000-638178/61.
 XX
 PT Novel p53 tumor suppressor gene encoding a protein useful for
 PT genetically modifying metazoan invertebrate organisms, such as insects
 PT for screening compounds of pharmaceutical use or a pesticide
 PS
 PS Example 7; Page 80-89; 98pp; English.
 XX
 CC Insect p53 tumour suppressor genes can be used to genetically modify
 CC metazoan invertebrate organisms, such as insects and worms, or
 CC cultured cells, resulting in p53 expression or mis-expression. The
 CC tumour suppressor genes, a p53 polypeptide or genetically modified
 CC organisms or cells are used in screening assays to identify compounds
 CC or molecules, preferably a pharmaceutical agent or a pesticide, that
 CC modulates p53 activity. The genetically modified organisms or cells
 CC are also useful for studying p53 activity by detecting the phenotype
 CC caused by the expression or mis-expression of the p53 protein in the
 CC insect. The method additionally comprises observing a second insect
 CC having the same genetic modification as the previous one, which
 CC causes the expression or mis-expression of the p53 protein, where the
 CC second animal additionally comprises a mutation in a desired gene and
 CC differences between the phenotype of the first and second identifies
 CC the desired gene as capable of modifying the function of the gene
 CC encoding the p53 protein. The genetically modified organisms or
 CC cells are also useful for identifying other genes modulating the
 CC function of, or interaction with the p53 gene.
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 Query Match 3.1%; Score 34.8; DB 21; Length 27425;
 Best Local Similarity 53.7%; Pred. No. 21; Mismatches 62; Indels 0; Gaps 0;
 Matches 72; Conservative 0; Mismatches 62; Indels 0; Gaps 0;
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 DB 4595 tgcctgagcgaacgagacaagacgcgtccgagcgcttcgcgcgctccatacgacg 4654
 OY 461 ttgaaaaatcgcaatctgtgtgatacgtgcttcgattgattgattacg 520
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 OY 521 aaccgaacgcgcgc 534
 DB 4715 agctgtacgccaac 4728

Search completed: May 7, 2002, 15:13:49
 Job time: 12250 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 7, 2002, 11:49:38 ; Search time 72.13 Seconds
(without alignments)
3871.971 Million cell updates/sec

Title: US-09-579-383-1
Perfect score: 1137
Sequence: 1 atgaatttaccgtaataaata.....tcgtgaagcctgcactaa 1137

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33.4	2.9	2149	1 US-08-784-651-3	Sequence 3, Appl
2	33.4	2.9	7218	1 US-08-222-463-14	Sequence 14, Appl
3	33	2.9	3533	2 US-08-476-062A-40	Sequence 40, Appl
4	33	2.9	3533	5 PCT-US96-01314-40	Sequence 40, Appl
5	33	2.9	5424399-1	Patent No. 5424399	Sequence 7, Appl
6	33	2.9	4080	1 US-08-570-311-7	Sequence 7, Appl
7	33	2.9	4080	2 US-08-353-485-7	Sequence 7, Appl
8	33	2.9	4510	1 US-08-570-311-1	Sequence 1, Appl
9	33	2.9	4510	2 US-08-353-485-1	Sequence 1, Appl
10	33	2.9	6241	1 US-08-570-311-25	Sequence 25, Appl
11	33	2.9	6895	1 US-08-570-311-9	Sequence 9, Appl
12	33	2.9	6895	2 US-08-353-485-9	Sequence 9, Appl
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14	33	2.9	7266	3 US-08-822-324-5	Sequence 5, Appl
15	33	2.9	7266	4 US-08-450-931-9	Sequence 9, Appl
16	33	2.9	8640	1 US-08-570-311-28	Sequence 28, Appl
17	32.6	2.9	5163	3 US-08-700-651-1	Sequence 1, Appl
18	32.6	2.9	5163	3 US-08-928-361B-4	Sequence 4, Appl
19	32.6	2.9	5318	3 US-08-700-651-2	Sequence 2, Appl
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22	32.4	2.8	2277	1 US-08-676-974-2	Sequence 2, Appl
23	32.4	2.8	2277	2 US-09-098-487-2	Sequence 2, Appl
24	32.2	2.8	2657	2 US-08-974-565C-8	Sequence 8, Appl
25	32.2	2.8	2657	3 US-09-255-748-8	Sequence 8, Appl
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37	30.8	2.7	1414	1 US-08-224-930-3	Sequence 3, Appl
38	30.8	2.7	3139	1 US-07-894-212A-1	Sequence 1, Appl
39	30.6	2.7	633	4 US-08-998-416-161	Sequence 161, App
40	30.6	2.7	4849	2 US-08-540-804-13	Sequence 13, Appl
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42	30.6	2.7	4849	3 US-08-521-872-13	Sequence 13, Appl
43	30.6	2.7	4849	4 US-08-590-399-13	Sequence 13, Appl
44	30.6	2.7	6418	1 US-08-480-528A-11	Sequence 11, Appl
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ALIGNMENTS

RESULT 1
US-08-784-651-3
: Sequence 3, Application US/08784651
: Patent No. 5821102
GENERAL INFORMATION:
: APPLICANT: Berka, Randy
: APPLICANT: Boomlathnan, Karuppan
: APPLICANT: Sandal, Thomas
: TITLE OF INVENTION: Nucleic Acids Encoding Polypeptides
: NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESSES:
: ADDRESS: 58211020 No. 5821102disk of No. 5821102th America, Inc.
: STREET: 405 Lexington Avenue
: CITY: New York
: STATE: NY
: COUNTRY: USA
: ZIP: 10174
COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/784,651
: FILING DATE: 21-JAN-1997
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Agtis, Cheryl H.
: REGISTRATION NUMBER: 34,086
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 212-867-0123
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2149 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: Genomic DNA
: US-08-784-651-3

Query Match 2.9%; Score 33.4; DB 1; Length 2149;
Best Local Similarity 54.5%; Pred. No. 0.91;
Matches 67; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 436 tccttgatctgactacacgcggttgaaataatcgaaatcgggtgatgaactggc 495
DB 1877 TCGTTCCTCATTCATTAATCTGTGTCATCAATCGTAATATCAATTAAGAAACAGG 1936

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QY      556   gaa 558  
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Db      1997 CAA 1999  
  
RESULT       2  
US-08-232-463-14/c  
; Sequence 14, Application US/08232463  
; Patent No. 5670367  
GENERAL INFORMATION:  
APPLICANT: DORNER, F.  
APPLICANT: SCHEIFLINGER, F.  
APPLICANT: PALKNER, F. G.  
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS  
NUMBER OF SEQUENCES: 52  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 1800 Diagonal Road, Suite 500  
CITY: Alexandria  
STATE: VA  
COUNTRY: USA  
ZIP: 22313-0299  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/232,463  
FILING DATE:  
CLASSIFICATION: .435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/935,313  
FILING DATE:  
APPLICATION NUMBER: EP 91 114 300.6  
FILING DATE: 26-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 30472/114 IMNU  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703)836-9300  
TELEFAX: (703)683-4109  
TELEX: 899149  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7218 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMEDIATE SOURCE:  
CLONE: PTZqpt-F15  
US-08-232-463-14
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NAME/KEY: Coding Sequence
LOCATION: 75...3530
US-08-476-062A-40

Query Match 2.9%; Score 33; DB 2; Length 3533;
Best Local Similarity 58.8%; Pred. No. 1.7;
Matches 57; Conservative 0; Mismatches 40; Indels 0; Gaps 0;
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DB 3470 GAAGCCGAGCTTGTACACGGCGGGGTGATGAGGCGCAGGACAGCACTCCCGACAGAGA 3411
OY 1084 ggcgcacataatgaacagctgtgcgactcgactctcg 1120
DB 3410 GCTGCCACGATGAGCGGCGGAGGGGTTGGGACCTCG 3374

RESULT 4
PCT-US96-01314-40/c
Sequence 40, Application PC/TUS9601314
GENERAL INFORMATION:
APPLICANT: M. Amin Arnaout
TITLE OF INVENTION: METHODS FOR IDENTIFYING INTEGRIN
NUMBER OF SEQUENCES: 78
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/01314
FILING DATE: 30-JAN-96
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/380,167
FILING DATE: 30-JAN-95
ATTORNEY/AGENT INFORMATION:
NAME: John W. Freeman
REGISTRATION NUMBER: 29,066
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 3533 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
PCT-US96-01314-40

Query Match 2.9%; Score 33; DB 5; Length 3533;
Best Local Similarity 58.8%; Pred. No. 1.7;
Matches 57; Conservative 0; Mismatches 40; Indels 0; Gaps 0;
OY 1024 gaaacaactgaataaacgcgcgaatggttcgacgtgtgtctctgtccagcgacaac 1083
DB 3470 GAAGCCGAGCTTGTACACGGCGGGGTGATGAGGCGCAGGACAGCACTCCCGACAGAGA 3411
OY 1084 ggcgcacataatgaacagctgtgcgactcgactctcg 1120
DB 3410 GCTGCCACGATGAGCGGCGGAGGGGTTGGGACCTCG 3374

RESULT 5
5424399-1/c
Patent No. 5424399
APPLICANT: ARNAOUT, M. AMIN
TITLE OF INVENTION: HUMAN CR3a/b HETERODIMERS
NUMBER OF SEQUENCES: 12
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/78,871
FILING DATE: 16-JUN-1993
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 539,842
FILING DATE: 18-JUN-1990
APPLICATION NUMBER: 212,573
FILING DATE: 28-JUN-1988
SEQ ID NO. 1:
LENGTH: 3533
5424399-1

Query Match 2.9%; Score 33; DB 6; Length 3533;
Best Local Similarity 58.8%; Pred. No. 1.7;
Matches 57; Conservative 0; Mismatches 40; Indels 0; Gaps 0;
OY 1024 gaaacaactgaataaacgcgcgaatggttcgacgtgtgtctctgtccagcgacaac 1083
DB 3470 GAAGCCGAGCTTGTACACGGCGGGGTGATGAGGCGCAGGACAGCACTCCCGACAGAGA 3411
OY 1084 ggcgcacataatgaacagctgtgcgactcgactctcg 1120
DB 3410 GCTGCCACGATGAGCGGCGGAGGGGTTGGGACCTCG 3374

RESULT 6
US-08-570-311-7
Sequence 7, Application US/08570311
Patent No. 5824791
GENERAL INFORMATION:
APPLICANT: Proguiske-Fox, Ann
APPLICANT: Tumwasorn, Somying
APPLICANT: Lepine, Guylaine
APPLICANT: Han, Naimeing
APPLICANT: Lantz, Marilyn
APPLICANT: Patil, Joseph
TITLE OF INVENTION: Cloned Porphyromonas gingivalis Genes
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ted W. Whitlock
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/570,311
FILING DATE:
CLASSIFICATION: 424
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/353,485
FILING DATE: 09-DEC-1994
CLASSIFICATION: 424
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/647,119
FILING DATE: 25-JAN-1991
CLASSIFICATION: 424
PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US 07/241,640
FILING DATE: 08-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UF15.C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
TELEFAX: (904) 372-5800
INFORMATION FOR SEQ. ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 4080 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 87..3347
US-08-570-311-7

Query Match 2.9%; Score 33; DB 1; Length 4080;
Best Local Similarity 48.2%; Pred. No. 1.9;
Matches 93; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

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DB 1877 AAAGTACTACTATGACGACGAGGTTTCCGGGGATACATGCGGTGATGATCTC 1936
QY 975 cccgaagcataaaatgctgtgtaaaatctatcgcgattcgtlaaaacttgaacaaact 1034
DB 1937 CAAGACGGGACGACGACGCCGAGACTTCACGTTGTTTGAAGAAACGCTTAACGGAAT 1996
QY 1035 gaataacgcgcagatggttcggtcgtgtgtctcttcacgcgacacgcggccataa 1094
DB 1997 AAATTAAGGGCGGACCAAGATTGGTCTTCCACGGAACCAATGGCCCAAACTCAAG 2056
QY 1095 tgaacagctgagc 1107
DB 2057 TGTATGATCGAG 2069

RESULT 7
US-08-353-485-7
Sequence 7, Application US/08353485
Patent No. 5830710
GENERAL INFORMATION:
APPLICANT: Proguiske-Fox, Ann
APPLICANT: Tumwasorn, Somying
APPLICANT: Lepine, Guylaine
APPLICANT: Han, Naiming
APPLICANT: Lantz, Marilyn
APPLICANT: Patti, Joseph
TITLE OF INVENTION: Cloned Porphyromonas gingivalis Genes
TITLE OF INVENTION: and Probes for the Detection of Periodontal Disease
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ted W. Whitlock
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/353,485
FILING DATE: 09-DEC-1994
CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/647,119
FILING DATE: 25-JAN-1991
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/241,640
FILING DATE: 08-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UF15.C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
TELEFAX: (904) 372-5800
INFORMATION FOR SEQ. ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 4080 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 87..3347
US-08-353-485-7

Query Match 2.9%; Score 33; DB 2; Length 4080;
Best Local Similarity 48.2%; Pred. No. 1.9; Mismatches 100; Indels 0; Gaps 0;
Matches 93; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

QY 915 aaagtaacgattacgtgcatcattcagcgttaccctgattgtcccgctcagccgttcaa 974
DB 1877 AAAGTACTACTATGACGACGAGGTTTCCGGGGATACATGCGGTGATGATCTC 1936
QY 975 cccgaagcataaaatgctgtgtaaaatctatcgcgattcgtlaaaacttgaacaaact 1034
DB 1937 CAAGACGGGACGACGACGCCGAGACTTCACGTTGTTTGAAGAAACGCTTAACGGAAT 1996
QY 1035 gaataacgcgcagatggttcggtcgtgtgtctcttcacgcgacacgcggccataa 1094
DB 1997 AAATTAAGGGCGGACCAAGATTGGTCTTCCACGGAACCAATGGCCCAAACTCAAG 2056
QY 1095 tgaacagctgagc 1107
DB 2057 TGTATGATCGAG 2069

RESULT 8
US-08-570-311-1
Sequence 1, Application US/08570311
Patent No. 5824791
GENERAL INFORMATION:
APPLICANT: Proguiske-Fox, Ann
APPLICANT: Tumwasorn, Somying
APPLICANT: Lepine, Guylaine
APPLICANT: Han, Naiming
APPLICANT: Lantz, Marilyn
APPLICANT: Patti, Joseph
TITLE OF INVENTION: Cloned Porphyromonas gingivalis Genes
TITLE OF INVENTION: and Probes for the Detection of Periodontal Disease
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ted W. Whitlock
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

Db 4457 CAAGCGGGCAGCAAGCGCCGAGACTTCACGGTGTTCGAAAGAAAGCCTAACGGAAAT 4516
 Oy 1035 gaataaagcgcaagatggcttcgagctgtgctctcgtccagcgcaagcgccataa 1094
 Db 4517 AAATAGGGCGGAGCAAGATTGCTCTTCCACGGAAGCAATGGCCCAACCTCAAG 4576
 Oy 1095 tgaacagctggcg 1107
 Db 4577 TGTATGATCGAG 4589

RESULT 12
 ; US-08-353-485-9
 ; Sequence 9, Application US/08353485
 ; Patent No. 5830710
 ; GENERAL INFORMATION:
 ; APPLICANT: Progulsk-Rox, Ann
 ; APPLICANT: Tumwasorn, Somying
 ; APPLICANT: Lepine, Guylaine
 ; APPLICANT: Han, Naiming
 ; APPLICANT: Lantz, Marilyn
 ; APPLICANT: Patti, Joseph
 ; TITLE OF INVENTION: Cloned Porphyromonas gingivalis Genes
 ; TITLE OF INVENTION: and Probes for the Detection of Periodontal Disease
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Ted W. Whitlock
 ; STREET: 2421 N.W. 41st Street, Suite A-1
 ; CITY: Gainesville
 ; STATE: FL
 ; COUNTRY: USA
 ; ZIP: 32606
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/353,485
 ; FILING DATE: 09-DEC-1994
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/647,119
 ; FILING DATE: 25-JAN-1991
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/241,640
 ; FILING DATE: 08-SEP-1988
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Whitlock, Ted W.
 ; REGISTRATION NUMBER: 36,965
 ; REFERENCE/DOCKET NUMBER: UP15.C2
 ; TELEPHONE: (904) 375-8100
 ; TELEFAX: (904) 372-5800
 ; INFORMATION FOR SEQ ID NO: 9:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 6895 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 696..5894
 ; US-08-353-485-9

Query Match 2.9%; Score 33; DB 2; Length 6895;
 Best Local Similarity 48.2%; Pred. No. 2.7;
 Matches 93; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

Oy 915 aaagtaagattacgtatcatcatatggtgctcaacctgatgttccggtccagcggttaa 974
 Db 4397 AAAGTACTACTATGACCAACGACGAGTGTTCCTCCGGGATCACTATAGGGTATGATCTC 4456
 Oy 975 ccgagacataaataatgcggttaaatatcatatcggtgattcgtaaaactgaaact 1034
 Db 4457 CAAGCGGGCAGCAAGCGCCGAGACTTCACGGTGTTCGAAAGAAAGCCTAACGGAAAT 4516
 Oy 1035 gaataaagcgcaagatggcttcgagctgtgctctcgtccagcgcaagcgccataa 1094
 Db 4517 AAATAGGGCGGAGCAAGATTGCTCTTCCACGGAAGCAATGGCCCAACCTCAAG 4576
 Oy 1095 tgaacagctggcg 1107
 Db 4577 TGTATGATCGAG 4589

RESULT 13
 ; US-08-336-308A-9
 ; Sequence 9, Application US/08336308A
 ; Patent No. 6017532
 ; GENERAL INFORMATION:
 ; APPLICANT: Travis, James
 ; APPLICANT: Potempa, Jan S.
 ; APPLICANT: Barr, Philip J.
 ; APPLICANT: Pavloff, Nadine
 ; TITLE OF INVENTION: Porphyromonas gingivalis
 ; TITLE OF INVENTION: Arginine-specific Proteinase Coding Sequences
 ; NUMBER OF SEQUENCES: 16
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Greenlee, Wanner and Sullivan, P.C.
 ; STREET: 5370 Manhattan Circle, Suite 201
 ; CITY: Boulder
 ; STATE: Colorado
 ; COUNTRY: US
 ; ZIP: 80303
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/336,308A
 ; FILING DATE: 08-NOV-1994
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/119,361
 ; FILING DATE: 10-SEP-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/265,441
 ; FILING DATE: 24-JUN-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Feather, Donna M.
 ; REGISTRATION NUMBER: 33,878
 ; REFERENCE/DOCKET NUMBER: 21-93C
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (303) 499-8080
 ; TELEFAX: (303) 499-8089
 ; INFORMATION FOR SEQ ID NO: 9:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 7266 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; HYPOTHEICAL: NO
 ; ANTI-SENSE: NO
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 949..6063
 ; US-08-336-308A-9

LOCATION: 949...6063
US-08-822-324-5

MODECODE LIFE, NO
HYPOTHETICAL: NO

ANTI-SENSE: NO

FEATURE:
NAME/KEY: CDS
LOCATION: 949..6063
US-09-490-931-9

Query Match 2.98; Score 33; DB 4; Length 7266;
Best Local Similarity 48.28; Pred. No. 2.7;
Matches 93; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

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QY 975 cccgacgataaaatgctgttaaatctatcgcgcatlctgtaaaaactgaaacaaact 1034
Db 4650 CAAGACGGGGCGACGACGCGGACTTCACGGTTGTTTCGAGAAAGCCCTAAGGGAAT 4709
QY 1035 gaataaacgcgcagatgttctggcctgtgtctctgtccagcgacaacgcgcgccataa 1094
Db 4710 AAATTAAGGGCGGACAGATTCGGTTTCCACGGAAGCCAAATGCGGCCAAACCTCAAAG 4769
QY 1095 tgaacagctggcg 1107
Db 4770 TGTATGGATCGAG 4782

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Job time: 11991 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 7, 2002, 11:49:38 ; Search time 1778.63 Seconds
(without alignments)
8628.010 Million cell updates/sec

Title: US-09-579-383-1
Perfect score: 1137
Sequence: 1 atgaatttaccgtaaata.....tcgtgaagcctgcactaa 1137

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues
Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_estl:*
10: gb_estl2:*
11: gb_hic:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inu:*
15: em_gss_pln:*
16: em_gss_vrl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
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2	39.6	3.5	563	10 B1514040	B1514040 B160014A
3	39.6	3.5	598	10 B1504891	B1504891 B170014A
4	38.4	3.4	600	10 B1989791	B1989791 4051-42 M
5	38.4	3.4	725	10 B6911261	B6911261 602807526
6	38.4	3.4	772	10 B1110193	B1110193 602900608
7	38.4	3.4	963	10 BE573275	BE573275 601333173
8	38	3.3	799	10 BG973651	BG973651 602844687
9	37.4	3.3	465	10 B1512890	B1512890 B160010B
10	37.4	3.3	475	10 B1516075	B1516075 B160021A
11	36.8	3.2	851	12 CENS00A0A	AL055901 DROSOPH11
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13	36.2	3.2	316	12 CENS007VF	AL050885 DROSOPH11
14	36.2	3.2	401	10 BG126386	BG126386 EST472032
15	36.2	3.2	407	12 AO902979	AO902979 GSSC0786
16	36.2	3.2	703	12 AO357632	AO357632 CITR-RI-
17	36.2	3.2	716	10 B1926776	B1926776 EST346665

18	36.2	3.2	719	10 B1926607	B1926607 EST546496
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21	36	3.2	809	12 BH310912	BH310912 CH230-129
22	36	3.2	898	9 AU176209	AU176209 AU176209
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25	35.8	3.1	923	12 A2543048	A2543048 ENTRB61TR
26	35.4	3.1	995	12 CENS00731	AL066753 DROSOPH11
27	35.2	3.1	625	9 BB633589	BB633589 BB633589
28	35.2	3.1	632	10 BG080114	BG080114 H3049H03-
29	35.2	3.1	655	9 BB625765	BB625765 BB625765
30	35.2	3.1	679	9 BB642408	BB642408 BB642408
31	35.2	3.1	782	9 AU080792	AU080792 AU080792
32	35.2	3.1	844	9 A1663310	A1663310 UK27D05.Y
33	35.2	3.1	933	10 BF975265	BF975265 602244773
34	35.2	3.1	1809	11 AK009954	AK009954 Mus muscu
35	35	3.1	680	9 AU169979	AU169979 AU169979
36	35	3.1	1101	12 CENS002EE	AL062399 DROSOPH11
37	34.8	3.1	389	9 A1956552	A1956552 u178f10.Y
38	34.8	3.1	468	9 AM011984	AM011984 um05b04.Y
39	34.8	3.1	481	9 A1930233	A1930233 u162a07.Y
40	34.8	3.1	486	9 AM227070	AM227070 um64g08.Y
41	34.8	3.1	506	10 W48324	W48324 mc85c07.r1
42	34.8	3.1	543	9 AA289281	AA289281 uc92D06.r
43	34.8	3.1	565	9 A1036742	A1036742 uc90b02.Y
44	34.8	3.1	575	10 BF786668	BF786668 60211428
45	34.8	3.1	597	9 AM318758	AM318758 um05h11.Y

ALIGNMENTS

RESULT 1
LOCUS B1514134 495 bp mRNA linear EST 29-AUG-2001
DEFINITION B160014A21A12 Bee Brain Normalized Library, B16 Apis mellifera
ACCESSION B1514134
VERSION B1514134
KEYWORDS cDNA clone B160014A21A12 5', mRNA sequence.
SOURCE B1514134.1 GI:15364508
ORGANISM honeybee
Apis mellifera
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata
; Apoidea; Apidae; Apis.
1 (bases 1 to 495)
Whitefield,C.W., Soares,B., Robertson,H.M., Pardinas,J., Liu,L.,
Smoller,D., and Robinson,G.E.
An Expressed Sequence Tag Resource for Studies of Brain and
Behavior in the Honey Bee
Unpublished (2001)
Contact: Gene E. Robinson
Department of Entomology
University of Illinois
505 S. Goodwin Ave., Urbana, IL 61801, USA
Tel: 217 265 0309
Fax: 217 244 3499
Email: generobi@life.uiuc.edu

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
This research was funded by the University of Illinois Critical
Research Initiatives Fund and a Burroughs-Wellcome Trust Innovation
Award in Functional Genomics to G.E. Robinson and an NSF
Postdoctoral Fellowship in Bioinformatics to C.W. Whitefield.
PCR Primers
FORWARD: TAATAGACTGACTATAGG
BACKWARD: ATTACCCCTACTAAG
Insert Length: 495 Std Error: 0.00
Plate: B160014A21 row: A column: 12
Seq primer: AGCGATACATTCACACAGCA
High quality sequence stop: 495.
Location/Qualifiers
1..495
/organism="Apis mellifera"

FEATURES
source

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/strain="mixed strains of European bees, predominantly
A.m. ligustica"
/cdo_xref="taxon:7460"
/clone="BB160014A21A12"
/clone_lib="Bee Brain Normalized Library, BB16"
/sex="female"
/tissue_type="brain"
/dev_stage="adult worker honey bee"
/lab_host="DH10B"
/notes="Origin: brain; Vector: pT73-Pac; Site:1: Ecor1;
Site-2: NotI; The BB16 library was contributed by the
Soares laboratory and it was constructed and normalized
as described by Bonaldo, M.F., Lennon, G. and Soares,
M.B. (1996). Genome Research 6(9): 791-806. RNA was
prepared from dissected brains of adult worker bees of
various ages and various behavioral groups."

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Query Match	3.5%	Score 39.6;	DB 10;	Length 495;
Best Local Similarity	47.6%;	Pred. No. 1.8;		
Matches 117; Conservative	0;	Mismatches 129;	Indels 0;	Gaps 0;

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Oy	918	gtacgattacgtatcatcatatggcgcttcacccctgatatgttcctcgctcaagccgttaacc	977
	85	ACTCACTTCAACAATCTCCAAAGCGTACAGATGGCTGTCCCATTTACGTGTGCCATTC	144

Oy 978 gaacgataaaatcgtcgtaaatctatctgcgatcttcgtaaaaaactgaaaacaaactgaa 103
||| ||| ||| ||| ||| ||| ||| |||
Db 145 ATTGGCACCACCGAATAATGAGCTCTTCGACTCCAAAGCAAGATCAAGACGCC 204

Oy 1038 taaacgcgcagatggttcgcgcctgtgtctctgtccagcgcacaacycgcccataatga 109

Db 205 TAATGACGGCAATGCACAATTCGTCCCTTCATCCAGCAGACAACATTTCGAGCAATGG 264

QY	1098	acagct	1103
Db	265	ATGAT	270

RESULT	2
LOCUS	B15140.40
DEFINITION	B15140.40 563 bp mRNA linear EST 29-AUG-2001
	B1600014A20A12 Bee Brain Normalized Library, B16 Apts mellifera
	CDNA clone B160014A20A12 5', mRNA sequence.

VERSION	BI514040.1	GI:15364414
KEYWORDS	EST.	
SOURCE	honeybee.	
ORGANISM	Apis mellifera	

REFERENCE

Pterygota: Neoptera: Endopterygota; Hymenoptera; Apocrita; Aculeata
; Apoidea; Apidae; Apis.
1 (bases 1 to 563)

Behavior in the Honey Bee
Unpublished (2001)
Contact: Gene E. Robinson

505 S. Goodwin Ave., Urbana, IL 61801, USA
Tel: 217 265 0309
Fax: 217 244 3499
Email: generobi@life.uiuc.edu
This research was funded by the University of Illinois Critical Research Initiatives Fund and a Burroughs-Wellcome Trust Innovation

Award in Functional Genomics to G.E. Robinson and an NSF Postdoctoral Fellowship in Bioinformatics to C.W. Whitfield

PCR primers

FORWARD: TATACGACGACACTATATAGG
BACKWARD: ATTAAACCCGACCTAAG

Insert Length: 563 Std Error: 0.00

Plate: BB16001A20 row: A column: 12

Seq primer: AGCGGATACCAATTCACACAGA

High quality sequence stop: 563.

Location/Qualifiers

1. 563

FEATURES

source

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/organism="Apis mellifera"
/strain="mixed strains of European bees, predominantly
A.m. ligustica"
/db_xref="taxon:7460"
/clone="BB16014A20A12"
/clone_lib="Bee Brain Normalized Library, BB16"
/sex="female"
/tissue_type="brain"
/dev_stage="adult worker honey bee"
/lab_host="BH10B"
/note="Organ: Brain; Vector: p7T73-Pac; Site_1: EcOR1,
Site_2: NotI; The BB16 library was contributed by the
Soares laboratory and it was constructed and normalized
as described by Bonaldo, M.F., Lennon, G., and Soares,
M.B. (1996), Genome Research 6(9): 791-806. RNA was
various ages and various behavioral groups."
BASE COUNT
158 a 135 g 135 t 2 others
ORIGIN

```

Query Match	3.5%	Score 39.6;	DB 10;	Length 563;
Best Local Similarity	47.6%;	Pred. No. 1.9;		
Matches 117; Conservative	0;	Mismatches 129;	Indels 0;	Gaps 0;

```

QY      858 ctctaccgaattctaccggtatgaagaattatacgaactccttcgcatactatgtaaaa 917
      ||| | ||||| |||| | ||||| | ||||| | |||||
Db      25 ctctgaagattctcgcgttttcgtgcacaatcagacacgacacgacacattcctcaatt 84

```

Oy 918 gtacgatttcgtgatcatcatatggcttcaacctgaagtctccgtccaacgcggtttcaacc 977
| | | | |
Db 85 acTcactTAcAAATACTCCAAACGGGTACAAGATGCGTGTCGATTCAATGCCTGCCAACC 144

D0 145 ATTGGGACCCCGCAGATTAATTAGACTCTTCGAAGTTCGAAAGAAGATCAAGACGGC 204

OY 1038 taacgcgcagatggttcgcgccttgcctcgtccagcgacaacgcggcccaatga 1097

QY 1098 acagct 1103
| | |

RESULT	3
B1504891	

ACCESSION BI504891
VERSION BI504891.1 GI:15355265
KEYWORDS EST.

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea; Apidae; Apis.
1 (bases 1 to 598)

Whitefield, C.W., Soares, B., Robertson, H.M., Pardinas, J.J., Liu, L., Smoller, D. and Robinson, G.E.

REFERENCE
AUTHORS

TITLE An Expressed Sequence Tag Resource for Studies of Brain and Behavior in the Honey Bee
JOURNAL Unpublished (2001)
COMMENT Contact: Gene F. Robinson
Department of Entomology
University of Illinois
505 S. Goodwin Ave., Urbana, IL 61801, USA
Tel: 217 245 0309
Fax: 217 244 3499
Email: genrob@life.uiuc.edu

This research was funded by the University of Illinois Critical Research Initiatives Fund and a Burroughs-Wellcome Trust Innovation Award in Functional Genomics to G.F. Robinson and an NSF Postdoctoral Fellowship in Bioinformatics to C.W. Whitfield.
PCR Primers
FORWARD: TAATGACCTCCTACTAGG
BACKWARD: ATTACCTCTCAATAGG

Insert Length: 598 Std Error: 0.00
Plate: BB170014A20 row: G column: 05
Seq primer: AGCGATACCAATTCACACGCA
High quality sequence stop: 598.

FEATURES
source Location/Qualifiers
1. 598
/organism="Apis mellifera"
/strain="mixed strains of European bees, predominantly A.m. ligustica"
/db_xref="taxon:7460"
/clone="BB170014A20C05"
/clone_lib="Bee Brain Normalized/Subtracted Library, BB17"
/sex="female"
/tissue_type="brain"
/dev_stage="adult worker honey bee"
/lab_host="DH10B"
/note="Organ: brain; Vector: pT73-Pac; Site: 1; ECoRI; Site 2: NotI; This BB17 cDNA library was generated by subtraction of the BB16 library with 4000 previously sequenced clones. The BB16 library was contributed by the Soares laboratory and it was constructed and normalized as described by Bonaldi, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-806. RNA was prepared from dissected brains of adult worker bees of various ages and various behavioral groups."

BASE COUNT 173 a 140 c 145 g 140 t
ORIGIN

Query Match 3.5%; Score 39.6; DB 10; Length 598;
Best Local Similarity 47.6%; Pred. No. 2;
Matches 117; Conservative 0; Mismatches 129; Indels 0; Gaps 0;
QY 858 ctctaccgattctaccgtatgaagaattatagcactctactatggttaaaa 917
DB 218 CTCGAGAGATCTCTCGTTTCGTCGACATACGACACGACGACATCTCAAT 277
QY 918 gtaagattagtcattcatcattggtgcttaccgtatgtccgcgtccgttcaacc 977
DB 278 ACTGACTTACAAATACCTCAACGCTACAGATGCTGTCGATCATGCTGCCATCC 337
QY 978 gaaagataaattgtctgtaaaattatctatcggtatgtttaaactgtaaaactctaa 1037
DB 338 ATTGCGGACCCCGACGAAATGAGCTCTTGCATCCAAAGGATCAAGGACCGCC 397
QY 1038 taacgagcagatggttcggtgctgtctctccagcgacaaacgagcccatatga 1097
DB 398 TAAAGACGGCAATGGCAACATTCGTGCGCTTCGATCCACGACAAACATTTGCAGCAATGG 457
QY 1098 acagct 1103
DB 458 ATGAT 463

RESULT 4
BI989791

LOCUS BI989791 600 bp mRNA linear EST 20-DEC-2001
DEFINITION 4051-42 Mouse E14.5 retina lambda ZAP II Library Mus musculus cDNA,
ACCESSION mRNA sequence.
VERSION BI989791
KEYWORDS BI989791.1 GI:17960794
SOURCE EST.
ORGANISM house mouse.
Mus musculus

REFERENCE
AUTHORS Mu, X., Zhao, S., Pershad, R., Hsieh, T.-F., Scarpa, A., Wang, S.W., White, R.A., Beremand, P.D., Thomas, T.L., Gan, L. and Klein, W.H.
TITLE Gene expression in the developing mouse retina by EST sequencing and microarray analysis
Nucleic Acids Res. 29 (24), 4983-4993 (2001)

JOURNAL
COMMENT Department of Biochemistry and Molecular Biology
University of Texas M.D. Anderson Cancer Center
Box 117, 1515 Holcombe Blvd., Houston, TX 77030, USA
Tel: 713 792 3646
Fax: 713 790 0329

FEATURES
source Location/Qualifiers
1. 600
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone_lib="Mouse E14.5 retina lambda ZAP II Library"
/tissue_type="neural retina"
/dev_stage="embryonic day 14.5 post-fertilization"
BASE COUNT 133 a 154 c 185 g 128 t
ORIGIN

Query Match 3.4%; Score 38.4; DB 10; Length 600;
Best Local Similarity 50.0%; Pred. No. 4.5;
Matches 96; Conservative 0; Mismatches 96; Indels 0; Gaps 0;
QY 674 acccgaaataatctgtatgtagtgcgaagctccgtatagcgaataattcaacaac 733
DB 275 ACCTGCAGACCCAGCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 334
QY 734 cggagcttaagaagaactgttaccgagcagccagatgagcatctgggtggtcatct 793
DB 335 AGCGCGAGGAAATGACATCTGACGCGGCTGTTGTATACCCGCTTGCGCATG 394
QY 794 acctatgacacacctgaaagatatgattgacatggttctgtgaggaattcaata 853
DB 395 ATCTGCAGCAGATGATCCAGCTGTGTGTGACACAGCTGACTGCGAGATGCCATGACC 454
QY 854 cgaactctaccg 865
DB 455 GAAAGACCCACAG 466

RESULT 5
BI911261
LOCUS BG911261 725 bp mRNA linear EST 05-JUN-2001
DEFINITION 602807526P1 NCI-GAP_Brn67 Homo sapiens cDNA clone IMAGE:4939710
5', mRNA sequence.
ACCESSION BG911261
VERSION BG911261.1 GI:14291737
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: David N. Louis, M.D.

CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
http://image.llnl.gov
Plate: LLM10877 row: c column: 07
High quality sequence stop: 721.
Location/Qualifiers
1..725

FEATURES
source
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4939710"
/clone_1lb="NCL_CGAP_Brn67"
/tissue_type="anaplastic oligodendroglioma with 1p/19q
loss"
/lab_host="DH10B (r1 phage-resistant)"
/note="Organ: brain; Vector: PCMV-SPORT6; Site_1: NCI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 2.3 kb. Constructed by Life
Technologies. Note: this is a NCL_CGAP Library."
BASE COUNT 150 a 206 c 236 g 133 t
ORIGIN

Query Match 3.4%; Score 38.4; DB 10; Length 725;
Best Local Similarity 60.6%; Pred. No. 4.9;
Matches 63; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

Qy 762 agcccgatgcatctgaggtgtgtgcatctactatgaacacccgaagatatgat 821
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 586 AGCCCAAGTGAACCTCGGAGGAGGAGGTGTACAGACATACAGCTGTGATGTCT 645

Qy 822 tgacatgtgtgtgtgagacgttcaactacacgaactcaccg 865
||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 646 AGCCAGAGACCTGTGTGAGAGAACACGACACATACATACAG 689

RESULT 6 772 bp mRNA linear EST 26-JUN-2001
LOCUS B1110193
DEFINITION 602900608F1 NCL_CGAP_Mam5 Mus musculus cDNA clone IMAGE:5030617 5',
mRNA sequence.
ACCESSION B1110193
VERSION B1110193.1 GI:14561094
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 772)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabds-remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
http://image.llnl.gov
Plate: LLM1085 row: o column: 02
High quality sequence stop: 759.
Location/Qualifiers
1..772

FEATURES
source
/organism="Mus musculus"
/strain="C57/B6"
/db_xref="taxon:10090"
/clone="IMAGE:5030617"
/clone_1lb="NCL_CGAP_Mam5"
/tissue_type="tumor, gross tissue"

/dev_stage="7 months"
/lab_host="DH10B"
/note="Organ: mammary; Vector: PCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Robin Humphreys,
NIH"

BASE COUNT 182 a 195 c 229 g 166 t
ORIGIN

Query Match 3.4%; Score 38.4; DB 10; Length 772;
Best Local Similarity 50.0%; Pred. No. 5;
Matches 96; Conservative 0; Mismatches 96; Indels 0; Gaps 0;
Qy 674 accggaataaatctgtgtgtagcaggaagtcgcgtataacgaagaatattcaacaac 733
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 264 ACTCTGACAGACCCACTGGGAGGAGGAGGTGTACAGACATACAGCTGTGAGGAAAC 323
Qy 734 cgaacgttaagaagaactgttacgcgagccagatgacatctgcggtgtgtcactc 793
||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 324 AGCCGAGAGAGATGACATCTGGACGGGGCTGTCTGTGATACCCGTGGCTTCTGGCAGTG 383
Qy 794 accgtatgaacacactggaagatatgatacattgacatggtgtgtgtgacagcttaactaca 853
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 384 ATCTGACAGACATGATCCAGGCTGTGTGTGACACAGCTGTACTGACATGCTCCATGACC 443
Qy 854 cgaactcaccg 865
||| ||| |||||
Db 444 GAAAGACCACAG 455

RESULT 7 963 bp mRNA linear EST 15-AUG-2000
LOCUS BE573275
DEFINITION 601333173F2 NCL_CGAP_Mam6 Mus musculus cDNA clone IMAGE:3710491 5',
mRNA sequence.
ACCESSION BE573275
VERSION BE573275.1 GI:9816995
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 963)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabds-remail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
http://image.llnl.gov
Plate: LLM8933 row: a column: 20
High quality sequence stop: 655.
Location/Qualifiers
1..963

FEATURES
source
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:3710491"
/clone_1lb="NCL_CGAP_Mam6"
/sex="female, virgin"
/tissue_type="infiltrating ductal carcinoma"
/dev_stage="5 months"
/lab_host="DH10B"
/note="Organ: mammary; Vector: PCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigators

BASE COUNT 255 a 233 c 285 g 190 t
ORIGIN providing samples: Jeffrey Green, M.D., NIH

Query Match 3.4%; Score 38.4; DB 10; Length 963;
Best Local Similarity 50.0%; Pred. No. 5.5;
Matches 96; Conservative 0; Mismatches 96; Indels 0; Gaps 0;

Qy 674 accggaanaaatctgtatgtatgtacgaagctccgtataacagaanaatttcaacaac 733
Db 22 ACCGTGACAGCCACTGGAGAGAGAGAGTGTACGACGACATCATGCTGTGAGAAAC 81
Qy 734 cgcagcgttaagaagaactgttacgcgcagccagatggcatctgcgggtggccatct 793
Db 82 AGGCCGAGGAAGATGACATCTGACGGGCGCTGTCTGATACCCGTGCTTGTGCAATG 141
Qy 794 accgtatgaacaacctgaagaatatgtatgacatgtgtgttgcacagcttaactaca 853
Db 142 ATCTGACAGCATGATGATCCAGCTGTGGTGCACACGTCTACTGCGAGATGCCATGACC 201
Qy 854 cgaactctaccg 865
Db 202 GAAAGACCACAG 213

RESULT 8 799 bp mRNA linear EST 12-JUN-2001
LOCUS BG973651
DEFINITION 602844687F1 NIH_CGAP_Mam4 Mus musculus cDNA IMAGE:4960308 5',
mRNA sequence.
ACCESSION BG973651
VERSION BG973651.1 GI:14361288
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE 1 (bases 1 to 799)
JOURNAL NIH-MGC http://mgc.nci.nih.gov/
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaaps-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth
Ph.D.

CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
http://image.lnl.gov
Plate: LLAM10979 row: n column: 21
High quality sequence stop: 797.
Location/Qualifiers

FEATURES
source 1..799
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:4960308"
/clone_1ib="NIH_CGAP_Mam4"
/tissue_type="tumor, gross tissue"
/lab_host="DH10B"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: oligo dT.
Average insert 2.5 kb. Library constructed by Life
Technologies, catalog # 12018-016. Investigators providing
samples: Lothar Hennighausen/Priscilla Furth, NIH
Reference for transgenic model: Li et al., Cell Growth and
Differentiation 7, 3-11 (1996). Note: this is a NCI_CGAP
Library."

BASE COUNT 181 a 207 c 238 g 173 t
ORIGIN

Query Match 3.3%; Score 38; DB 10; Length 799;
Best Local Similarity 50.0%; Pred. No. 6.7;
Matches 95; Conservative 0; Mismatches 95; Indels 0; Gaps 0;

Qy 674 accggaanaaatctgtatgtatgtacgaagctccgtataacagaanaatttcaacaac 733
Db 306 ACCGTGACAGCCACTGGAGAGAGAGTGTACGACGACATCATGCTGTGAGAAAC 365
Qy 734 cgcagcgttaagaagaactgttacgcgcagccagatggcatctgcgggtggccatct 793
Db 366 AGGCCGAGGAAGATGACATCTGACGGGCGCTGTCTGATACCCGTGCTTGTGCAATG 425
Qy 794 accgtatgaacaacctgaagaatatgtatgacatgtgtgttgcacagcttaactaca 853
Db 426 ATCTGACAGCATGATGATCCAGCTGTGGTGCACACGTCTACTGCGAGATGCCATGACC 485
Qy 854 cgaactctac 863
Db 486 GAAAGACCAC 495

RESULT 9 465 bp mRNA linear EST 29-AUG-2001
LOCUS B1512890
DEFINITION B160010B10B03 Bee Brain Normalized Library, B16 Apis mellifera
CDNA clone B160010B10B03 5', mRNA sequence.
ACCESSION B1512890
VERSION B1512890.1 GI:15363264
KEYWORDS EST.
SOURCE honeybee.
ORGANISM Apis mellifera

REFERENCE Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
AUTHORS Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata
TITLE 1 (bases 1 to 465)
JOURNAL Apidae; Apis.
COMMENT Whitfield, C.W., Soares, B., Robertson, H.M., Pardinas, J., Liu, L.,
Smoller, D. and Robinson, G.E.
An Expressed Sequence Tag Resource for Studies of Brain and
Behavior in the Honey Bee
Unpublished (2001)
Contact: Gene E. Robinson
Department of Entomology
University of Illinois
505 S. Goodwin Ave., Urbana, IL 61801, USA
Tel: 217 265 0309
Fax: 217 244 3499
Email: genetrob@life.uiuc.edu

This research was funded by the University of Illinois Critical
Research Initiatives Fund and a Burroughs-Wellcome Trust Innovation
Award in Functional Genomics to G.E. Robinson and an NSF
Postdoctoral Fellowship in Bioinformatics to C.W. Whitfield.
PCR Primers
FORWARD: TAATACGACTCACTATAGGG
BACKWARD: ATTAACTCTCACTAAG
Insert Length: 465 Std Error: 0.00
Plate: B160010B10 row: B column: 03
Seq primer: AGCGATACACATTTCCACACGGA
High quality sequence stop: 465.
Location/Qualifiers

FEATURES
source 1..465
/organism="Apis mellifera"
/strain="mixed strains of European bees, predominantly
A.m. ligustica"
/db_xref="taxon:7460"
/clone="B160010B10B03"
/clone_1ib="Bee Brain Normalized Library, B16"
/sex="female"
/tissue_type="brain"
/dev_stage="adult worker honey bee"
/lab_host="DH10B"
/note="Organ: brain; Vector: pT73-Pac; Site_1: EcoRI;
Site_2: NotI; The B16 Library was contributed by the

[illegible]

DB	623	GAAGCTGCTGCTGATTACCTTACAGCTTCAAGGCCAGTGGCCGCCACGATTTGGG	682
Qy	340	ctgaatgagtaactcaatgaatgacatgaatctgcgcaaaagctgcgcggaattattatg	399
Db	683	TGGGTGCTGCTTCTTTCTGCTGATTTAATGCTTACATCAGTACATGTAACAACAGCTGTGGA	742
Qy	400	ctgtcgtgagcctggcgcggtgtagaacctaccatccgcctccctctcgtatctgcgaactaacgcg	459
Db	743	AGCTCAGAGCTTGAGGAGTGAAGCTTCTGAGGCTTTGGCCATTATCCAGCCCAAAAGATTTC	802
Qy	460	gttgaaaaaatcgcaatctgltgtagtaacctgcggccttcgatgfatgtatgtagattac	519
Db	803	GTGGCTGCTGAGCTTACGTCTGTTGATGAGGAGCTGGGGAGAGAAAGATTGCTTGAATT	862
Qy	520	gaa 522	
Db	863	GAA 865	
RESULT	13		
CNS007VF	316 bp	DNA	linear
LOCUS			
DEFINITION	CNS007VF	316 bp	DNA
LOCUS			
DEFINITION	BACR1B12 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.		
ACCESSION	AL050885		
VERSION	AL050885.1		
KEYWORDS	GSS.		
SOURCE	fruit fly,		
ORGANISM	Drosophila melanogaster.		
	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.		
REFERENCE	Genoscope.		
AUTHORS	Direct Submission		
TITLE	Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :		
JOURNAL	BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)		
COMMENT	Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mamoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain Y2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm .		
FEATURES	Location/Qualifiers		
source	1..316		
	/organism="Drosophila melanogaster"		
	/db_xref="taxon:7227"		
	/clone_lib="RPCI-98"		
	/clone="BACR1B12"		
	/note="end : TET3"		
BASE COUNT	120 a 32 c 40 g 48 t 76 others		
ORIGIN			
Query Match	3.2%	Score 36.2;	DB 12; Length 316;
Best Local Similarity	38.4%;	Pred. No. 15;	
Matches	68; Conservative 26; Mismatches 83; Indels 0; Gaps 0;		
Qy	865	gattctaccgttatagaagaattatagacctccctacgatatctatgtaaaaaagtagat	924
Db	3	GANNANNACCACTTRNGCATCAGTCAGCAGCAARWGGAGTGCAGATAAAMWMTAAACGAR	92

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 7, 2002, 15:13:52 ; Search time 2185.39 Seconds
(without alignments)
10887.518 Million cell updates/sec

Title: US-09-579-383-1

Perfect score: 1137

Sequence: 1 atgaatttaccgtaataa.....tcgtgaagcctgcactaa 1137

Scoring table: OLIGO NWC
Gapop 60.0 , Gapext 60.0

Searched: 1797656 seqs, 10463268293 residues

Word size : 0
Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

- GenEmbl:*
- 1: gb_da:*
- 2: gb_htg:*
- 3: gb_in:*
- 4: gb_om:*
- 5: gb_ov:*
- 6: gb_pat:*
- 7: gb_ph:*
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- 12: gb_sy:*
- 13: gb_un:*
- 14: gb_vl:*
- 15: em_da:*
- 16: em_fun:*
- 17: em_hum:*
- 18: em_in:*
- 19: em_jnu:*
- 20: em_om:*
- 21: em_or:*
- 22: em_ov:*
- 23: em_pat:*
- 24: em_ph:*
- 25: em_pl:*
- 26: em_ro:*
- 27: em_sts:*
- 28: em_un:*
- 29: em_vl:*
- 30: em_htg_hum:*
- 31: em_htg_in:*
- 32: em_htg_other:*
- 33: em_htg_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Match Length	ID	Description
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68	3			
69	3			
70	3			
71	3			
72	3			
73	3			

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2	22	1.9	630	10	AF361355	AF361355 Rattus no
3	22	1.9	2122	6	AX079087	AX079087 Sequence
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5	22	1.9	142978	9	AC097717	AC097717 Homo sapi
6	7	1.9	168415	30	AC012529	AC012529 Homo sapi
7	22	1.8	173998	2	AC108032	AC108032 Homo sapi
8	21	1.8	132388	2	AC108190	AC108190 Felis cat
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15	20	1.8	636	10	MMU272046	MMU272046 Mus muscu
16	20	1.8	712	3	AF353629	AF353629 Trypanoso
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19	20	1.8	740	3	AF353628	AF353628 Trypanoso
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34	20	1.8	156265	20	AC079140	AC079140 Homo sapi
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38	20	1.8	174189	9	AC068185	AC068185 Homo sapi
39	20	1.8	176495	2	AC087215	AC087215 Papio cyn
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62	19	1.7	4093	1	AF083352	AF083352 Helicobac
63	19	1.7	12621	1	AE008621	AE008621 Rickettsia
64	19	1.7	20674	1	AE008854	AE008854 Salmonella
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67	19	1.7	29885	9	AC093679	AC093679 Homo sapi
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70	19	1.7	37412	2	AC107008	AC107008 Rattus no
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DEFINITION Rattus norvegicus voltage-dependent calcium channel gamma
subunit-like protein mRNA, complete cds.
ACCESSION AF361355
VERSION AF361355
KEYWORDS AF361355.1 GI:17974543
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 630)
AUTHORS Chu, P.-J., Robertson, H.M. and Best, P.M.
TITLE Calcium channel gamma subunits provide insights into the evolution
of this gene family
JOURNAL Gene 280 (1-2), 37-48 (2001)
PUBMED 11738816
REFERENCE 2 (bases 1 to 630)
AUTHORS Chu, P.-J., Robertson, H. and Best, P.M.
TITLE Direct Submission
JOURNAL Submitted (14-MAR-2001) Department of Molecular and Integrative
Physiology, University of Illinois, 407 S. Goodwin Ave., Urbana, IL
61801, USA
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Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3
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LOCUS AX079087
DEFINITION Sequence 8 from Patent WO0107591.
ACCESSION AX079087
VERSION AX079087.1 GI:13158661
KEYWORDS Pseudomonas sp.
SOURCE Pseudomonas sp.
ORGANISM Pseudomonas sp.
Bacteria; Proteobacteria.
REFERENCE 1 (bases 1 to 2122)
AUTHORS Fraser, C.M., Venter, C., Tuemmler, B., Hohelsel, J., Duesterhoeft, A.,
Hilbert, H., Timms, K.N., Moore, E., Straetz, M. and Helm, S.
TITLE Data sequences which code export systems
JOURNAL Patent: WO 0107591-A 8 01-FEB-2001;
THE INSTITUTE FOR GENOMIC RESEARCH (US)
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source location/Qualifiers
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Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 2068 GCTGCTGAGCCTGGCGGTGAG 2089

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LOCUS AC027117
DEFINITION Homo sapiens chromosome 8 clone RP11-806011 map 8, LOW-PASS
SEQUENCE SAMPLING.
ACCESSION AC027117
VERSION AC027117.3 GI:11990735
KEYWORDS HTG; HTGS_PHASE0.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 69006)
AUTHORS Birren, B., Linton, L., Nusbaum, C. and Lander, E.
TITLE Homo sapiens chromosome 8, clone RP11-806011
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 69006)
AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F.,
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TITLE
JOURNAL
COMMENT

Boguslavskiy, L., Boukhgalter, B., Brown, A., Burkett, G.,
Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S.,
Collamore, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J. S.,
Dodge, S., Domino, M., Doyle, M., Ferreira, P., Fitzhugh, W., Gage, D.,
Galagan, J., Gardyna, S., Glinde, S., Coyette, M., Graham, L.,
Grand-Pierre, N., Grant, G., Hagos, B., Heatford, A., Horton, L.,
Howland, J. C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A.,
Klein, J., LaRoque, K., Lamazares, R., Landers, T., Lehoczy, J.,
Levine, R., Liu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N.,
McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R.,
Meldrum, J., Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J.,
Murphy, T., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P.,
O'Neill, D., Olivari, T. M., Oliver, J., Peterson, K., Pierre, N.,
Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D.,
Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B.,
Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
Teste, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J.,
Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J.,
Young, G., Zainoun, J., Zimmer, A. and Zody, W.

Direct Submission

Submitted (26-MAR-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Dec 23, 2000 this sequence version replaced gi:7705183.

All repeats were identified using RepeatMasker:

Smith, A.F.A. & Green, P. (1996-1997)

<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: MIBR

Web site: <http://www-seq.wi.mit.edu>

Contact: sequence_submissions@genome.wi.mit.edu

Project Information

Center Project name: L8867

Center Clone name: 806_O_11

* NOTE: This record contains 83 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.

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 DEFINITION Homo sapiens chromosome 2 clone RP11-650N19, complete sequence.
 ACCESSION AC097717 AC037452
 VERSION AC097717.3 GI:18072229
 KEYWORDS HTG.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE 1
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 TITLE 1 (bases 1 to 142978)
 JOURNAL Materston, R. H.
 The sequence of Homo sapiens clone

REFERENCE 2
 AUTHORS Unpublished
 TITLE 2 (bases 1 to 142978)
 JOURNAL Materston, R. H.
 Direct Submission
 Submitted (21-OCT-2001) Genome Sequencing Center, Washington
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,
 MO 63108, USA

REFERENCE 3
 AUTHORS 3 (bases 1 to 142978)
 TITLE Waterston, R. H.
 Direct Submission
 Submitted (06-JAN-2002) Genome Sequencing Center, Washington
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,

COMMENT MO 63108, USA
 On Jan 6, 2002 this sequence version replaced gi:16756374.

----- Genome Center -----
 Center: Washington University Genome Sequencing Center
 Center code: WUGSC
 Web site: http://genome.wustl.edu/gsc/index.shtml
 Contact: submissions@watson.wustl.edu
 ----- Project Information -----
 Center project name: H_NH0650N19
 Drafting center: WMR

FEATURES
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 /db_xref="taxon:9606"
 /chromosome="12"
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BASE COUNT 43068 a 28143 c 27230 g 44537 t
 ORIGIN

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 SV AC012529.2
 DT 02-NOV-1999 (Rel. 61, Created)
 DT 28-MAY-2000 (Rel. 63, Last updated, Version 3)
 DE Homo sapiens chromosome 2 clone RP11-106123 map 2, WORKING DRAFT SEQUENCE.
 DE 20 unordered pieces.
 XX HTG: HTGS_DRAFT; HTGS_PHASE1.
 XX Homo sapiens (human)
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
 CC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 XX [1]
 RP 1-168415
 RT "Homo sapiens chromosome 2, clone RP11-106123";
 RL Unpublished.

[2]
 RP 1-168415
 RA Birren B., Linton L., Nusbaum C., Lander E., Allen N., Anderson M.,
 Baldwin J., Barna N., Beckerly R., Boguslavsky L., Boukhgalter B.,
 Brown A., Castle A., Collange M., Collins S., Collins S., Cooke P.,
 Dearrellano K., Dewar K., Domino M., Donelan L., Doyle M., Ferreira P.,
 Fitzhugh W., Forrest C., Funke R., Gage D., Galagan J., Gardyna S.,
 Grant G., Hagos B., Heaford A., Horton L., Howland J.C., Johnson R.,
 Jones C., Kann L., Karatas A., Klein J., Lebecky J., Lien C., Locke K.,
 MacDonald P., Margulis N., McKernan P., McKernan K., McLaughlin J.,
 Meldrum J., Morrow J., Naylor J., Norman C.H., O'Connor T., O'Donnell P.,
 Peterson K., Pollara V., Riley R., Roy A., Santos R., Severy P.,
 Stange-Thomann N., Stojanovic N., Subramanian A., Talamas J., Tesfaye S.,
 Tirrell A., Vassiliev H., Vo A., Wheeler J., Wu X., Wyman D., Ye W.J.,
 RA Zimmer A., Zody M.;
 RT

SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
AUTHORS 1 (bases 1 to 173998)
TITLE The sequence of Homo sapiens clone
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 173998)
AUTHORS Waterston, R.H.
TITLE Submitted (24-JAN-2002) Genome Sequencing Center, Washington
JOURNAL University School of Medicine, 4444 Forest Park Parkway, St. Louis,
Mo 63108, USA
COMMENT On Jan 24, 2002 this sequence version replaced g1:8096824.

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
Contact: submissions@wustl.wustl.edu
Project Information -----
Center project name: H_NH0106123
Drafting center: WIBR

----- Summary Statistics -----
Sequencing vector: M13; %
Sequencing vector: plasmid; %
Chemistry: Dye-primer ET; % of reads
Chemistry: Dye-terminator Big Dye; % of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 171517 bases at least Q40
Consensus quality: 172379 bases at least Q30
Consensus quality: 173864 bases at least Q20
Insert size: 174000; agarose-fp
Insert size: 175963; sum-of-coverage
Quality coverage: 7.60 in Q20 bases; agarose-fp
Quality coverage: 7.52 in Q20 bases; sum-of-coverage

* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

* 1 61739: contig of 61739 bp in length
* 61740 61839: gap of unknown length
* 61840 173998: contig of 112159 bp in length.
Location/Qualifiers
1. 173998
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="2"
/clone="RP11-106123"
1. 61739
/note="assembly_name:Contig26
clone_end:SP6
vector_side:left"
61840. 173998
/note="assembly_name:Contig27
vector_side:left"
clone_end:SP6
misc_feature
61840. 173998
/note="assembly_name:Contig27
vector_side:left"
clone_end:SP6
BASE COUNT 53651 a 33484 c 34031 g 52732 t 100 others
ORIGIN

Query Match 1.9%; Score 22; DB 2; Length 173998;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1017 aaaaactgaacaactgcat 1038

Db 103229 AAAAAGTGAACAACTGAT 103250
|||||
RESULT 8
AC108190
LOCUS
DEFINITION
AC108190
ACCESSION
AC108190
VERSION
AC108190.1 GI:18376889
KEYWORDS
HTG; HTGS_PHASE2; HTGS_DRAFT.
SOURCE
ORGANISM
Felis catus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
REFERENCE 1 (bases 1 to 132388)
AUTHORS Akhter, N., Ayale, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
Blakesley, R.W., Bouffard, G.G., Green, K., Brinkley, C., Brooks, S.,
Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,
Ho, S.-L., Idol, J.R., Karling, E., Latic, P., Lee-Lin, S.-O.,
Legaspi, R., Maduro, Q.L., Maduro, V.B., Masfello, C., Maskeri, B.,
Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Prasad, A.,
Stantipop, S., Thomas, J.W., Thomas, P.J., Touchman, J.W.,
Tsurgon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
Young, A., Zhang, L.-H. and Green, E.D.
NISC Comparative Sequencing Initiative
Unpublished
2 (bases 1 to 132388)
Green, E.D.
Direct Submission
Submitted (26-JAN-2002) NIH Intramural Sequencing Center, 8717
Groommont Circle, Galtersburg, MD 20877, USA
COMMENT ----- Genome Center -----
Center: NIH Intramural Sequencing Center
Center code: NISC
Web site: http://www.nisc.nih.gov
Contact: nisc_mouseingrl.nih.gov
Project Information
Center project name: cod
Center clone name: 443102

----- Summary Statistics -----
Sequencing vector: plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 132360 bases at least Q40
Consensus quality: 132380 bases at least Q30
Consensus quality: 132388 bases at least Q20
Insert size: 134000; agarose-fp
Insert size: 132388; sum-of-coverage
Quality coverage: 11.04x in Q20 bases; agarose-fp
Quality coverage: 11.18x in Q20 bases; sum-of-coverage

* NOTE: This is a 'working draft' sequence. It currently
* consists of 1 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

* 1 132388: contig of 132388 bp in length.
Location/Qualifiers
1. 132388
/organism="Felis catus"
/db_xref="taxon:9685"
/clone="RP86-44312"
/clone_id="RP86"
1. 132388
/note="assembly-fragment
clone_end:SP6
vector_side:left"

FEATURES
source
misc_feature

BASE COUNT 42519 a 25354 c 24854 g 39661 t
ORIGIN
Query Match 1.88; Score 21; DB 2; Length 132388;
Best Local Similarity 100.0%; Pred. No. 6.2;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1016 taaaactgaacaaactga 1036
Db 33965 TAAAACTGAACAACTGA 33985
RESULT 9
AC097081 138247 bp DNA linear HTG 20-DEC-2001
LOCUS Rattus norvegicus clone CH230-49G13, *** SEQUENCING IN PROGRESS
DEFINITION *** 59 unordered pieces.
ACCESSION AC097081.3 GI:17973481
VERSION AC097081
KEYWORDS HTG: HTGS PHASE1.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 138247)
Muzny,D.M., Adams,C., Adlo-Oduola,B., Ali-Osman,F.R., Allen,C.,
Alsbrooks,S.L., Amaratunga,H.C., Are,J.R., Banks,T., Barbatta,
Benton,D., Bimaye,K., Blankenhorn,K., Bonnin,D., Bouck,U.,
Bowle,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C.,
Burck,P., Burkett,C., Burrell,K.L., Byrd,N.C., Caron,T.F.,
Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R.,
Chen,Z., Chowdhury,I., Christopoulos,C., Cleveland,C.D., Cox,C.,
Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C.,
Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delaper,H.,
Deum,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H.,
Dugan-Rocha,S., Durbin,K.J., Earhart,C., Edgar,D., Edwards,C.C.,
Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J.,
Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T.,
Garza,N., Gill,R., Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S.,
Hamilton,K., Harris,C., Harris,K., Hart,M., Haylak,P., Hawes,A.,
Hernandez,J., Hernandez,O., Hodgson,A., Hogues,M., Hollaway,C.,
Hollins,B., Homsl,F., Howard,S., Huber,J., Huliyk,S., Hume,J.,
Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S.,
Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J.,
Kovar,C., Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C.,
Lewis,L., Li,J., Li,Z., Licharge,O., Lieu,C., Liu,J., Liu,W.,
Louisege,H., Lozano,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R.,
Ma,J., Maheshwari,M., Mapua,P., Martin,R., Martindale,A.,
Martinez,E., Massey,E., Mawhinney,E., McLeod,M.P., Meador,M.,
Mel,G., Metzger,M., Miner,G., Miner,Z., Mitchell,J., Mottabatt,K.,
Morgan,M., Morris,S., Moser,M., Neal,D., Newton,J., Newton,N.,
Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Nwokkwo,S.,
Ogun,M., Okwuonu,G., Oragunye,N., Oviedo,R., Pace,A., Payton,B.,
Peery,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L.L.,
Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojibokan,I., Rolfe,M.,
Ruiz,S., Savery,G., Scherer,S., Scott,G., Shen,H., Shoochhari,N.,
Slison,I., Sodergren,E., Sonaike,T., Sparks,A., Stanley,H.,
Stone,H., Sutton,A., Svatek,A., Tabor,P., Tameris,A., Tameris,K.,
Tang,H., Tansey,J., Taylor,C., Taylor,T., Tellrod,B., Thomas,N.,
Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalón,D., Vinson,R.,
Wall,R., Wang,S., Ward-Moore,S., Warren,R., Washington,C.,
Washington,S., Williams,G., Williamson,A., Wleczek,R., Wooden,S.,
Worley,K., Wu,C., Wu,X., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
Weinstock,G., and Gibbs,R.
TITLE Direct Submission
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 138247)
AUTHORS Worley,K.C.
TITLE Direct Submission
JOURNAL Submitted (09-OCT-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One

COMMENT

Baylor Plaza, Houston, TX 77030, USA
On Dec 20, 2001 this sequence version replaced gi:17064380.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GHXN
Center clone name: CH230-49G13
----- Summary Statistics
Assembly program: Phrap; version 0.990329first call to
findPhrapList
Consensus quality: 110444 bases at least Q40
Consensus quality: 117693 bases at least Q30
Consensus quality: 124112 bases at least Q20
Estimated insert size: 111960; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; agarose-1p estimation
Quality coverage: 1.5x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 59 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1
* 7367: contig of 7367 bp in length
* 7368
* 7467: gap of unknown length
* 7468
* 13890: contig of 6423 bp in length
* 13891
* 13990: gap of unknown length
* 13991
* 18960: contig of 4970 bp in length
* 18961
* 19060: gap of unknown length
* 23333: contig of 4273 bp in length
* 23334
* 24433: gap of unknown length
* 25881: contig of 2448 bp in length
* 25882
* 25981: gap of unknown length
* 30421: contig of 4440 bp in length
* 30521: gap of unknown length
* 32693: contig of 2174 bp in length
* 32696
* 32795: gap of unknown length
* 32796
* 36270: contig of 3475 bp in length
* 36271
* 36370: gap of unknown length
* 40217: contig of 3847 bp in length
* 40218
* 40317: gap of unknown length
* 42903: contig of 2586 bp in length
* 43003: gap of unknown length
* 43004
* 46231: contig of 3228 bp in length
* 46232
* 46331: gap of unknown length
* 49308: contig of 2977 bp in length
* 49309
* 49408: gap of unknown length
* 51457: contig of 2049 bp in length
* 51458
* 53950: gap of unknown length
* 53951
* 54050: gap of unknown length
* 56239: contig of 2189 bp in length
* 56240
* 56339: gap of unknown length
* 58280: contig of 1941 bp in length
* 58380: gap of unknown length
* 60968: contig of 2588 bp in length
* 61068: gap of unknown length
* 64015: gap of unknown length
* 64016
* 64115: gap of unknown length
* 67209: contig of 3094 bp in length
* 67210
* 67309: gap of unknown length
* 69958: contig of 2649 bp in length
* 69959
* 70058: gap of unknown length
* 70059
* 71538: contig of 1480 bp in length
* 71539
* 71638: gap of unknown length
* 73427: contig of 1789 bp in length

```

* 73428 73527: gap of unknown length
* 73528 76068: contig of 2541 bp in length
* 76069 76168: gap of unknown length
* 76169 79477: contig of 3309 bp in length
* 79478 79577: gap of unknown length
* 79578 81785: contig of 2208 bp in length
* 81786 81885: gap of unknown length
* 81886 83753: contig of 1868 bp in length
* 83754 83853: gap of unknown length
* 83854 86171: contig of 2318 bp in length
* 86172 86271: gap of unknown length
* 86272 87499: contig of 1228 bp in length
* 87500 87599: gap of unknown length
* 87600 89038: contig of 1439 bp in length
* 89039 89138: gap of unknown length
* 89139 92546: contig of 3408 bp in length
* 92547 92549: gap of unknown length
* 92549 95159: contig of 2513 bp in length
* 95160 95259: gap of unknown length
* 95260 96596: contig of 1337 bp in length
* 96597 96696: gap of unknown length
* 96697 98116: contig of 1420 bp in length
* 98117 98216: gap of unknown length
* 98217 98622: contig of 1406 bp in length
* 98623 99722: gap of unknown length
* 99723 101221: contig of 1499 bp in length
* 101222 101321: gap of unknown length
* 101322 102454: contig of 1133 bp in length
* 102455 102554: gap of unknown length
* 102555 103839: contig of 1285 bp in length
* 103840 103939: gap of unknown length
* 103940 105230: contig of 1291 bp in length
* 105231 105330: gap of unknown length
* 105331 107000: contig of 1670 bp in length
* 107001 107100: gap of unknown length
* 107101 108797: contig of 1697 bp in length
* 108798 108897: gap of unknown length
* 108898 110317: contig of 1420 bp in length
* 110318 110417: gap of unknown length
* 110418 112498: contig of 2081 bp in length
* 112499 112598: gap of unknown length
* 112599 114388: contig of 1790 bp in length
* 114389 114488: gap of unknown length
* 114489 115691: contig of 1203 bp in length
* 115692 115791: gap of unknown length
* 115792 117646: contig of 1855 bp in length
* 117647 117746: gap of unknown length
* 117747 118865: contig of 1119 bp in length
* 118866 118965: gap of unknown length
* 118966 120061: contig of 1096 bp in length
* 120062 120161: gap of unknown length
* 120162 121287: contig of 1126 bp in length
* 121288 121387: gap of unknown length
* 121388 123004: contig of 1617 bp in length
* 123005 123104: gap of unknown length
* 123105 124973: contig of 1859 bp in length
* 124974 125073: gap of unknown length
* 125074 126303: contig of 1230 bp in length
* 126304 126403: gap of unknown length
* 126404 127649: contig of 1246 bp in length
* 127650 127749: gap of unknown length
* 127750 129482: contig of 1733 bp in length
* 129483 129582: gap of unknown length
* 129583 130645: contig of 1063 bp in length
* 130646 130745: gap of unknown length
* 130746 132461: contig of 1716 bp in length
* 132462 132561: gap of unknown length
* 132562 134179: contig of 1618 bp in length
* 134180 134279: gap of unknown length

```

Query Match 1.8% Score 21: DB 2: Length 138247;
 Best Local Similarity 100.0% Pred. No. 6.2;
 Matches 21: Conservative 0: Mismatches 0: Indels 0: Gaps 0;

Qy 311 aaagcctgattgctgcgagt 331
 Db 14375 AAAGCCTGATTGCTGCAGT 14355

RESULT 10
 AC108193 139411 bp DNA linear HTG 26-JAN-2002
 AC108193/C Felis catus clone RP86-469M8, WORKING DRAFT SEQUENCE, 2 unordered
 LOCUS pieces.

DEFINITION
 AC108193.1 GI:18376892
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Felis catus

REFERENCE
 AUTHORS
 1 (bases 1 to 139411)
 Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.

TITLE
 JOURNAL
 REFERENCE
 AUTHORS
 JOURNAL
 COMMENT
 Submitted (26-JAN-2002) NIH Intramural Sequencing Center, 8717
 Grovemont Circle, Gaithersburg, MD 20877, USA

Center: NIH Intramural Sequencing Center
 Center code: NISC
 Web site: http://www.nisc.nih.gov
 Contact: nisc.mouse@bgrl.nih.gov
 Project Information

Center project name: coe
 Center clone name: 469M08
 Summary Statistics
 Sequencing vector: plasmid; n/a; 100% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.990319
 Consensus quality: 138590 bases at least Q40
 Consensus quality: 138720 bases at least Q30
 Consensus quality: 138869 bases at least Q20
 Insert size: 133000; agarose-fp
 Insert size: 139311; sum-of-contigs
 Quality coverage: 12.22x in Q20 bases; agarose-fp
 Quality coverage: 11.66x in Q20 bases; sum-of-contigs

NOTE: This is a 'working draft' sequence. It currently
 consists of 2 contigs. The true order of the pieces
 is not known and their order in this sequence record is
 arbitrary. Gaps between the contigs are represented as
 runs of N, but the exact sizes of the gaps are unknown.
 This record will be updated with the finished sequence
 as soon as it is available and the accession number will
 be preserved.

1 33148: contig of 33148 bp in length
 * 33149 33248: gap of unknown length
 * 33249 139411: contig of 106163 bp in length.
 Location/Qualifiers
 1. 139411

FEATURES
 source
 /organism="Felis catus"
 /db_xref="taxon:9685"
 /clone="RP86-469M8"
 /clone_lib="RP86"
 misc_feature
 1. 33148


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misc_feature      22605..22805
                  /note="match to EST AA502194 (MID:g2237161) ng73e12.sl"
misc_feature      22605..22805
                  /note="match to EST AA502194 (MID:g1847487) nc11g07.rl"
misc_feature      22609..22808
                  /note="match to EST AA484674 (MID:g2211468) ne64a03.sl"
gene              22780..29226
                  /gene="NPY"
                  /complement(join(22780..22804,24888..24968,29039..29226))
                  /gene="NPY"
                  /note="match to protein P01303 (PID:g128117):
                  H_RG18R13.1"
                  /codon_start=1
                  /product="neuropeptide Y precursor"
                  /protein_id="AAC08287.1"
                  /db_xref="gi:2992498"
                  /translation="MLGNKRRLGSLGTLALSLVLCALAEAYPSKPNPGDAPEAD
                  MARYSALRHYINILTRQRYGRSSPELIDLMRESTENVPRILEDPAWM"
repeat_region     23527..23690
                  /rpt_family="Alu"
misc_feature      24859..24970
                  /note="match to EST AA662702 (MID:g2616693) nv06h11.sl"
misc_feature      24859..24970
                  /complement(24859..24970)
                  /gene="NPY"
                  /note="match to EST AA226171 (MID:g1847487) nc11g07.rl"
misc_feature      24859..24970
                  /note="match to EST AA502194 (MID:g2237161) ng73e12.sl"
repeat_region     26493..26667
                  /rpt_family="MERL_type"
repeat_region     26686..26872
                  /rpt_family="MERL_type"
repeat_region     28886..28964
                  /rpt_family="L2"
misc_feature      29006..30527
                  /note="Cpg_island (%GC=65.4, o/e=0.80, #cpgs=123)"
misc_feature      29037..29223
                  /note="match to EST AA662702 (MID:g2616693) nv06h11.sl"
repeat_region     32483..33035
                  /rpt_family="L1"
repeat_region     33034..33965
                  /rpt_family="L1"
repeat_region     34024..34394
                  /rpt_family="MALR"
repeat_region     34395..34584
                  /rpt_family="L1"
repeat_region     35069..35311
                  /rpt_family="L2"
repeat_region     35345..41477
                  /rpt_family="L1"
repeat_region     41729..42145
                  /rpt_family="MALR"
repeat_region     42234..42446
                  /rpt_family="MERL_type"
repeat_region     42807..42990
                  /rpt_family="L2"
repeat_region     43879..44184
                  /rpt_family="Alu"
repeat_region     44664..44934
                  /rpt_family="Alu"
repeat_region     45003..45251
                  /rpt_family="L1"
repeat_region     45338..45585
                  /rpt_family="L2"
repeat_region     45623..46229
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repeat_region     46230..46277
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repeat_region     46278..46504
                  /rpt_family="L2"
repeat_region     46517..46674
                  /rpt_family="L1"
repeat_region     46715..46852
                  /rpt_family="MERL_type"
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repeat_region     47387..47478
                  /rpt_family="L1"
repeat_region     47824..48086
Query Match      1.8%: Score 21; DB 9; Length 185516;
Best Local Similarity 100.0%; Pred No. 6.2;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 794 accgatgaacacacgtaag 814
|||||
DB 49017 ACCTGATGAACACCTGANAAG 48997
|||||
RESULT 12
AL596170 313450 bp DNA linear BCT 04-DEC-2001
LOCUS Listeria innocua Clp11262 complete genome, segment 8/12.
DEFINITION AL596170 AL592022
ACCESSION AL596170.1 GI:16414292
VERSION
KEYWORDS
SOURCE
ORGANISM
Listeria innocua.
Listeria innocua
Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Listeria.
1 (sites)
REFERENCE
AUTHORS Glaser,P., Frangeul,L., Buchrieser,C., Rusniok,C., Amend,A.,
Bagero,F., Berche,P., Bloeker,H., Brandt,P., Chakraborty,T.,
Charbit,A., Chetoui,F., Couve,E., de Daruvar,A., Deloux,P.,
Domann,E., Dominguez-Bernal,G., Duchaud,E., Durant,L.,
Dussurget,O., Entian,K.D., Esnault,H., Portillo,F.G., Garrido,P.,
Gautier,L., Goebel,N., Gomez-Lopez,N., Hain,T., Hain,U.,
Jackson,D., Jones,L.M., Kaerst,U., Kreft,J., Kuhn,M., Kunst,F.,
Kurapat,G., Madueno,E., Maitournon,A., Vicente,J.M., Ng,B.,
Nedjari,H., Nordstedt,G., Novella,S., de Pablo,B., Perez-Diaz,J.C.,
Purcell,R., Remmel,B., Rose,M., Schlieter,T., Simoes,N.,
Tierrez,A., Vazquez-Boland,J.A., Voss,H., Weiland,U. and Cossart,P.
Comparative genomes of Listeria species
Science 294 (5543), 849-852 (2001)
2 (bases 1 to 313450)
JOURNAL Glaser,P., Frangeul,L. and Rusniok,C.
REFERENCE Direct Submission
AUTHORS Submitted (09-JUL-2001) Glaser P., Institut Pasteur, Genomique des
Microorganismes Pathogenes, 25 rue du Docteur Roux, 75724 Paris
Cedex 15, FRANCE
COMMENT E-mail: pglaser@pasteur.fr
Phone: +33 (0)1 45 68 89 96, Fax: +33 (0)1 45 68 87 86.
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RESULT 14

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pseudogene, exon 2, partial sequence.
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AF182790
VERSION
AF182790.1 GI:6525126
KEYWORDS
SOURCE
Pueraria phaseoloides.
ORGANISM
Pueraria phaseoloides
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Pueraria.
REFERENCE
1 (bases 1 to 573)
Adams,K.L., Song,K., Roessler,P.G., Nugent,J.M., Doyle,J.L.,
Doyle,J.J. and Palmer,J.D.
Intracellular gene transfer in action: dual transcription and
multiple silencings of nuclear and mitochondrial cox2 genes in
legumes
Proc. Natl. Acad. Sci. U.S.A. 96 (24), 13863-13868 (1999)
JOURNAL
MEDLINE
20040642
REFERENCE
2 (bases 1 to 573)
Song,K.
Direct Submission
Submitted (02-SEP-1999) Biology, Indiana University, Jordan Hall
142, 1001 E. Third St., Bloomington, IN 47405, USA
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ACCESSION
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VERSION
AJ272046.1 GI:7452297
CAACNG5 gene; calcium channel gamma 5 subunit.
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ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
Klugbauer,N., Dai,S., Specht,V., Lacinova,L., Marels,E., Bohn,G.
and Hofmann,F.
A family of gamma-like calcium channel subunits
FEBS Lett. 470 (2), 189-197 (2000)
JOURNAL
MEDLINE
20200313
REFERENCE
2 (bases 1 to 636)
Klugbauer,N.
Direct Submission
Submitted (08-FEB-2000) Klugbauer N., Institut fuer Pharmakologie

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und Toxikologie, Technische Universitaet Muenchen, Biedersteiner Str. 29, 81827 Muenchen, GERMANY

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CDS

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

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(without alignments)
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Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 1736436 seqs, 858457221 residues

Word size: 0

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

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Post-processing: Listing first 1000 summaries

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SUMMARIES

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4	19	1.7	882	24	AAK61604
5	19	1.7	1282	21	AAC50729
6	19	1.7	1289	21	AAC40124
7	18	1.6	453	18	AAV74939
8	18	1.6	581	22	ABA63976
9	18	1.6	581	22	ABA31149

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c 11	18	1.6	581	22	AAK38184	Human bone marrow
c 12	18	1.6	581	22	AAI18978	Probe #8911 for ge
c 13	18	1.6	581	22	AAI44114	Probe #12800 used
c 14	18	1.6	694	21	AAE12222	Aspergillus oryzae
c 15	18	1.6	1396	22	AAI58814	Human cDNA encodin
c 16	18	1.6	1684	23	ABL09429	Drosophila melanog
c 17	18	1.6	1858	22	AAE81761	Human membrane ass
c 18	18	1.6	1911	23	ABL02868	Drosophila melanog
c 19	18	1.6	1961	22	ABA6173	Human breast cell
c 20	18	1.6	1961	22	ABA56719	Human foetal liver
c 21	18	1.6	1961	22	AAI19984	Probe #4917 for ge
c 22	18	1.6	1961	22	AAI36330	Probe #5016 used t
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c 24	18	1.6	1986	22	ABA56714	Human foetal liver
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c 26	18	1.6	1986	22	AAK06844	Human brain expres
c 27	18	1.6	1986	22	AAI14980	Probe #4913 for ge
c 28	18	1.6	1986	22	AAI36326	Probe #5012 used t
c 29	18	1.6	1986	22	AAI04747	Probe #4738 used t
c 30	18	1.6	2081	21	AAE78399	Human secreted pro
c 31	18	1.6	2334	22	ABA51285	Human breast cell
c 32	18	1.6	2334	22	ABA69293	Human foetal liver
c 33	18	1.6	2334	22	AAI24172	Probe #14105 for g
c 34	18	1.6	2334	22	AAI49459	Probe #18145 used
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c 36	18	1.6	2351	22	ABA69288	Human foetal liver
c 37	18	1.6	2351	22	ABA36214	Probe #14680 for g
c 38	18	1.6	2351	22	AAK17575	Human brain expres
c 39	18	1.6	2351	22	AAI24168	Probe #14101 for g
c 40	18	1.6	2351	22	AAI49455	Probe #18141 used
c 41	18	1.6	2351	22	AAI09732	Probe #9723 used t
c 42	18	1.6	2723	23	ABL26896	Drosophila melanog
c 43	18	1.6	3164	21	AAE58979	Human cytoskeletal
c 44	18	1.6	3263	23	AAE84443	DNA encoding novel
c 45	18	1.6	3416	13	AAQ21004	Dex receptor prote
c 46	18	1.6	4258	18	ABL18134	Drosophila melanog
c 47	18	1.6	4419	22	AAD06838	Human STRAP-3 cDNA
c 48	18	1.6	4429	22	AAD07073	Human six transmem
c 49	18	1.6	6614	20	AAE26905	6.6 kb transcript
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c 51	18	1.6	11131	23	ABL09428	Drosophila melanog
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c 53	18	1.6	16092	23	ABL05124	Human digestive sy
c 54	18	1.6	31952	22	AAK89370	Human reproductive
c 55	18	1.6	32250	22	AAI06975	Tumour suppressor
c 56	18	1.6	38342	22	AAE46745	Human secreted exp
c 57	17	1.5	188	21	AAE41572	Human cancer cell
c 58	17	1.5	269	21	AAE16548	Human protein enco
c 59	17	1.5	300	20	AAE98380	Human nervous syst
c 60	17	1.5	314	22	AAE99757	zebra mays DNA fragm
c 61	17	1.5	351	22	ABA16776	DNA encoding a Sta
c 62	17	1.5	479	21	AAE40951	Neisseria meningit
c 63	17	1.5	615	18	AAE84082	Neisseria meningit
c 64	17	1.5	696	22	AAE56442	Neisseria meningit
c 65	17	1.5	696	22	AAE56443	Neisseria meningit
c 66	17	1.5	696	22	AAE56444	Neisseria meningit
c 67	17	1.5	696	22	AAE56445	Neisseria meningit
c 68	17	1.5	696	22	AAE56446	Neisseria meningit
c 69	17	1.5	696	22	AAE56447	Neisseria meningit
c 70	17	1.5	696	22	AAE56448	Neisseria meningit
c 71	17	1.5	696	22	AAE56449	Neisseria meningit
c 72	17	1.5	696	22	AAE56450	Neisseria meningit
c 73	17	1.5	696	22	AAE56451	Neisseria meningit
c 74	17	1.5	696	22	AAE56452	Neisseria meningit
c 75	17	1.5	696	22	AAE56453	Neisseria meningit
c 76	17	1.5	696	22	AAE56454	Neisseria meningit
c 77	17	1.5	714	21	AAE05483	Streptococcus pneu
c 78	17	1.5	747	21	AAE291827	Human neuroblastom
c 79	17	1.5	809	22	AAI22553	Human breast cance
c 80	17	1.5	849	22	AAE84605	E. coli growth and
c 81	17	1.5	880	23	ABL16495	Drosophila melanog

c	83	17	1.5	924	22	AA57408	Human immune/haema
c	84	17	1.5	942	22	AAH74584	Synthetic nucleoti
c	85	17	1.5	957	14	AAO51347	c424 gene. Asperg
c	86	17	1.5	969	20	AAI19904	Streptococcus pneu
c	87	17	1.5	1016	23	ABLO7413	Drosophila melanog
c	88	17	1.5	1022	22	AAH29068	Drosophila melanog
c	89	17	1.5	1035	21	AAI34605	Arabidopsis thalia
c	90	17	1.5	1114	22	ABA49026	Human breast cell
c	91	17	1.5	1114	22	ABA34028	Probe #12494 for g
c	92	17	1.5	1114	22	AAI5385	Human brain expres
c	93	17	1.5	1114	22	AAK41110	Human bone marrow
c	94	17	1.5	1114	22	AAI21874	Probe #11807 for g
c	95	17	1.5	1114	22	AAI07562	Probe #7553 used t
c	96	17	1.5	1177	21	AAI1665	Arabidopsis thalia
c	97	17	1.5	1226	22	AAI91718	Human pollinosis-a
c	98	17	1.5	1370	19	AAZ96377	S. pneumoniae deri
c	99	17	1.5	1383	23	AAI81021	DNA encoding novel
c	100	17	1.5	1480	22	ABA43927	Human breast cell
c	101	17	1.5	1480	22	ABA24160	Probe #2626 for ge
c	102	17	1.5	1490	22	AAK02675	Human bone marrow
c	103	17	1.5	1490	22	AAI28113	Probe #2623 for ge
c	104	17	1.5	1490	22	AAI12690	Probe #2590 used t
c	105	17	1.5	1490	22	AAI02599	DNA encoding novel
c	106	17	1.5	1600	23	AA572685	WO 99/07855 SeqID
c	107	17	1.5	1627	20	AAI22980	Human polynucleoti
c	108	17	1.5	1630	22	AAI59400	Human polynucleoti
c	109	17	1.5	1662	20	AAI2899	WO 99/07855 SeqID
c	110	17	1.5	1668	22	AAI61186	Human polynucleoti
c	111	17	1.5	1668	22	AAI61187	Human polynucleoti
c	112	17	1.5	1666	23	ABLO8451	Drosophila melanog
c	113	17	1.5	1696	23	AA584426	DNA encoding novel
c	114	17	1.5	1759	22	AAI59401	Human polynucleoti
c	115	17	1.5	1780	21	AAI41739	Arabidopsis thalia
c	116	17	1.5	1988	21	AAK03309	Human brain expres
c	117	17	1.5	2193	21	AAI68671	Rat R35 CDNA. Rat
c	118	17	1.5	2565	21	AAI9175	Human pollinosis-a
c	119	17	1.5	2558	21	AAI21637	Human breast and o
c	120	17	1.5	2686	12	AAO10163	Cyclomatidoxetin
c	121	17	1.5	2687	11	AAO01792	Sequence encoding
c	122	17	1.5	2863	11	AAO05631	Lambda gtl0ch2 enc
c	123	17	1.5	2976	21	AAI26914	Essential Staphylo
c	124	17	1.5	2976	22	AAI08065	Staphylococcus aur
c	125	17	1.5	2976	22	AAI17705	Human cDNA sequenc
c	126	17	1.5	2976	22	AAI91596	Staphylococcus aur
c	127	17	1.5	3194	23	ABLO7412	Drosophila melanog
c	128	17	1.5	3217	23	ABLI6494	Drosophila melanog
c	129	17	1.5	3274	23	ABLI9018	Drosophila melanog
c	130	17	1.5	3316	11	AAO05632	Lambda gtl0ch101 e
c	131	17	1.5	3516	22	AAK85421	Human immune/haema
c	132	17	1.5	3527	23	ABLO9309	Drosophila melanog
c	133	17	1.5	3688	11	AAO05630	Lambda gtl0ch201 e
c	134	17	1.5	3703	13	AAO20200	Gene encoding C-te
c	135	17	1.5	3712	23	ABLO7600	Drosophila melanog
c	136	17	1.5	3746	10	AAI90693	Bovine peptidyl-gl
c	137	17	1.5	3844	13	AAQ20199	Gene encoding C-te
c	138	17	1.5	3904	13	AAQ20198	Gene encoding C-te
c	139	17	1.5	3925	12	AAQ11041	Encodes equine C-t
c	140	17	1.5	4045	13	AAQ20197	Gene encoding C-te
c	141	17	1.5	4370	23	ABLO8450	Drosophila melanog
c	142	17	1.5	4563	24	AA594875	Human DNA sequence
c	143	17	1.5	4676	23	AA584690	DNA encoding novel
c	144	17	1.5	4732	22	AAK70267	Human immune/haema
c	145	17	1.5	5066	19	AAV52212	Streptococcus pneu
c	146	17	1.5	5137	18	AAV74528	Staphylococcus aur
c	147	17	1.5	5274	22	AAK6782	Human immune/haema
c	148	17	1.5	5420	23	ABLO27968	Drosophila melanog
c	149	17	1.5	5836	23	ABLO2526	Drosophila melanog
c	150	17	1.5	6231	23	ABLO9308	Drosophila melanog
c	151	17	1.5	6558	22	ABA21372	Human nervous syst
c	152	17	1.5	6558	22	AAI37138	Human musculoskele
c	153	17	1.5	6558	22	AAK86101	Human immune/haema
c	154	17	1.5	7953	18	AAV74463	Staphylococcus aur
c	155	17	1.5	8367	21	AAH81483	N. meningitidis pa
c	156	17	1.5	11093	23	ABLO2506	Drosophila melanog
c	157	17	1.5	24200	23	ABLI21182	Drosophila melanog
c	158	17	1.5	24206	23	ABLI21180	Drosophila melanog
c	159	17	1.5	24235	23	ABLO5026	Drosophila melanog
c	160	17	1.5	30889	23	ABLI9852	Drosophila melanog
c	161	17	1.5	31563	23	ABLO2738	Drosophila melanog
c	162	17	1.5	34094	20	AAI30165	Complete nucleotid
c	163	17	1.5	38189	23	ABLI9856	Drosophila melanog
c	164	17	1.5	39814	19	ABLI9854	Drosophila melanog
c	165	17	1.5	40352	23	AAV02032	MAGE-B cluster DNA
c	166	17	1.5	48974	20	AAI55300	Mouse Presentin-1
c	167	17	1.5	349980	21	AAI21544	Neisseria meningit
c	168	17	1.5	349980	21	AAI21607	Neisseria meningit
c	169	17	1.5	1437668	19	AAV81490	N. meningitidis B
c	170	17	1.5	164976	19	AAV21209	Methanococcus jan
c	171	17	1.4	163	22	AAI13911	5' UTR of yeast YA
c	172	17	1.4	178	22	AAI12977	Human secreted pro
c	173	17	1.4	187	21	AAI31265	Human bone marrow
c	174	17	1.4	193	22	AAI31355	Human secreted pro
c	175	17	1.4	230	21	AAI04981	Human secreted pro
c	176	17	1.4	231	24	AAI02677	CDNA sequence #464
c	177	17	1.4	248	16	AAI03948	Human MSR2 gene ex
c	178	17	1.4	248	16	ABLO1821	Human MSR2 (BMSH2)
c	179	17	1.4	251	16	AAI23682	Human gene signatu
c	180	17	1.4	251	16	AAI23682	Human breast cance
c	181	17	1.4	274	22	AAI12196	Human gene expres
c	182	17	1.4	296	20	AAI67567	Human gene expres
c	183	17	1.4	300	20	AAI14867	Human foetal liver
c	184	17	1.4	315	22	ABA70985	Probe #15869 for g
c	185	17	1.4	315	22	ABA37403	Human brain expres
c	186	17	1.4	315	22	AAI19261	Human bone marrow
c	187	17	1.4	315	22	AAI45231	Probe #15135 for g
c	188	17	1.4	315	22	AAI25202	Probe #1968 used
c	189	17	1.4	320	22	AAI51182	Human immune/haema
c	190	17	1.4	321	16	AAI57185	Human MSR2 gene PC
c	191	17	1.4	339	22	AAI03318	DNA encoding novel
c	192	17	1.4	339	22	AAI02009	Human reproductive
c	193	17	1.4	344	22	AAI63302	Human immune/haema
c	194	17	1.4	346	21	AAI67566	Eucalyptus grandis
c	195	17	1.4	359	21	AAI26658	Human secreted pro
c	196	17	1.4	370	21	AAI98933	Human pancreatic c
c	197	17	1.4	375	21	AAI40202	H. pylori 26 kDa p
c	198	17	1.4	377	22	AAI63027	Human immune/haema
c	199	17	1.4	385	22	AAI21079	Human breast cance
c	200	17	1.4	391	21	AAI26965	Human secreted pro
c	201	17	1.4	395	21	AAI26965	Human immune/haema
c	202	17	1.4	400	22	AAI82249	Human polynucleoti
c	203	17	1.4	401	22	AAI96258	Human neutrophilin g
c	204	17	1.4	401	22	AAI97751	Human neutrophilin g
c	205	17	1.4	402	22	AAI96724	Human neutrophilin g
c	206	17	1.4	402	22	AAI98217	Human immune/haema
c	207	17	1.4	402	22	AAI98217	Eucalyptus grandis
c	208	17	1.4	406	21	AAI98217	Human immune/haema
c	209	17	1.4	426	21	AAI98217	Human immune/haema
c	210	17	1.4	426	22	AAI98217	Human immune/haema
c	211	17	1.4	431	22	AAI98217	Human immune/haema
c	212	17	1.4	440	23	AAI98217	DNA encoding novel
c	213	17	1.4	445	22	AAI98217	Novel human polynu
c	214	17	1.4	451	22	AAI98217	Human bone marrow
c	215	17	1.4	455	22	AAI98217	Human foetal liver
c	216	17	1.4	455	22	AAI98217	Probe #5964 for ge
c	217	17	1.4	455	22	AAI98217	Human bone marrow
c	218	17	1.4	455	22	AAI98217	Human brain expres
c	219	17	1.4	455	22	AAI98217	Human bone marrow
c	220	17	1.4	455	22	AAI98217	Probe #5918 for ge
c	221	17	1.4	455	22	AAI98217	Probe #6710 used t
c	222	17	1.4	456	22	AAI98217	Human immune/haema
c	223	17	1.4	475	22	AAI98217	Human foetal liver
c	224	17	1.4	475	22	AAI98217	Human foetal liver
c	225	17	1.4	475	22	AAI98217	Probe #244 for gen
c	226	17	1.4	475	22	AAI98217	Probe #245 for gen
c	227	17	1.4	475	22	AAI98217	Human brain expres
c	228	17	1.4	475	22	AAI98217	Human brain expres
c	229	17	1.4	475	22	AAI98217	Human bone marrow

229	16	1.4	475	22	AAK25688	Human bone marrow
230	16	1.4	475	22	AAI10315	Probe #248 for gen
231	16	1.4	475	22	AAI10316	Probe #249 for gen
232	16	1.4	475	22	AAI31568	Probe #254 used to
233	16	1.4	475	22	AAI31569	Probe #255 used to
234	16	1.4	475	22	AAI00251	Probe #242 used to
235	16	1.4	475	22	AAI00252	Probe #243 used to
236	16	1.4	480	20	AAV86552	EST clone AW170.
237	16	1.4	500	23	AAV76003	DNA encoding novel
238	16	1.4	538	22	AAI02558	Human reproductive
239	16	1.4	543	22	AAI34807	Human musculoskele
240	16	1.4	546	22	AAH35057	Human colon cancer
241	16	1.4	549	22	AAK56724	Human immune/haema
242	16	1.4	553	22	AAH10327	Human cDNA clone (
243	16	1.4	568	22	ABA06963	Human pancreatic c
244	16	1.4	568	22	AAK88162	Human digestive sy
245	16	1.4	582	22	AAK38542	Human bone marrow
246	16	1.4	589	22	AAK42810	Human G Protein-Co
247	16	1.4	589	22	AAK36030	Human bone marrow
248	16	1.4	593	22	ABA61912	Human foetal liver
249	16	1.4	593	22	AAK10222	Human brain expres
250	16	1.4	593	22	AAK36121	Human bone marrow
251	16	1.4	593	22	AAI14835	Probe #10521 used
252	16	1.4	618	18	AAV24658	H. pylori ORF 05cp
253	16	1.4	624	21	AAZ3841	RAB6c coding sequ
254	16	1.4	715	21	AAK50979	Arabidopsis thalia
255	16	1.4	718	21	AAZ38335	RAB6 coding sequen
256	16	1.4	721	21	AAK40852	Arabidopsis thalia
257	16	1.4	723	21	AAK63224	DNA encoding human
258	16	1.4	723	22	AAK91834	Human cDNA 5'-end
259	16	1.4	733	23	AAK52385	E. coli DNA for ce
260	16	1.4	739	21	AAZ38336	RAB6c coding sequ
261	16	1.4	740	21	AAZ38337	RAB6 coding sequen
262	16	1.4	747	23	AAK57116	DNA encoding novel
263	16	1.4	766	20	AAK39666	Renal cancer assoc
264	16	1.4	791	23	AAK72736	DNA encoding novel
265	16	1.4	793	22	AAK3184	Human cDNA clone r
266	16	1.4	798	23	AAK66629	DNA encoding novel
267	16	1.4	798	23	AAK76013	DNA encoding novel
268	16	1.4	798	23	AAK81257	DNA encoding novel
269	16	1.4	828	20	AAK61652	B. burgdorferi ant
270	16	1.4	833	22	AAK33006	DNA encoding novel
271	16	1.4	833	22	AAK33007	DNA encoding novel
272	16	1.4	849	18	AAV06127	Viral infection ge
273	16	1.4	860	20	AAK39911	Gastric cancer ass
274	16	1.4	873	20	AAK61651	B. burgdorferi ant
275	16	1.4	875	22	AAK57246	Corynebacterium gl
276	16	1.4	885	22	AAK53262	S. epidermidis ope
277	16	1.4	888	20	AAK57388	Rat U3 gene trap d
278	16	1.4	921	22	AAK42227	Human oxidoreducta
279	16	1.4	921	22	AAK42227	Sp5 mutant clone w
280	16	1.4	957	22	AAK31775	Human olfactory re
281	16	1.4	960	22	AAK42276	Human cDNA encodin
282	16	1.4	965	8	AAK70775	Sequence encoding
283	16	1.4	966	13	AAK29960	Sugar beet chitina
284	16	1.4	996	22	AAK29636	DNA encoding P. ae
285	16	1.4	1001	20	AAK03300	Partial cDNA encod
286	16	1.4	1001	22	AAK6934	Nucleotide sequenc
287	16	1.4	1065	22	AAK1894	Corynebacterium gl
288	16	1.4	1076	22	AAK59935	Human apoptosis-re
289	16	1.4	1110	22	AAK76036	DNA encoding spina
290	16	1.4	1158	18	AAK75411	Staphylococcus aur
291	16	1.4	1172	23	AAK70851	DNA encoding novel
292	16	1.4	1191	22	AAK44981	CDNA encoding nove
293	16	1.4	1197	22	AAK66530	Human pterio-molylb
294	16	1.4	1239	22	AAK68963	Human immune/haema
295	16	1.4	1247	13	AAK21978	Hybrid mini-vitel
296	16	1.4	1256	16	AAK91638	zebrafish sonic he
297	16	1.4	1256	16	AAK25621	zebrafish sonic he
298	16	1.4	1256	20	AAK25102	zebrafish sonic he
299	16	1.4	1256	20	AAK07275	zebrafish sonic he
300	16	1.4	1256	20	AAK16186	zebrafish Shh hedg
301	16	1.4	1256	21	AAK50450	zebrafish Sonic he
302	16	1.4	1256	21	AAK27880	zebrafish Sonic he
303	16	1.4	1256	21	AAK30278	Partial zebrafish
304	16	1.4	1256	21	AAK52261	zebrafish Sonic he
305	16	1.4	1256	22	AAK66775	zebrafish sonic he
306	16	1.4	1256	22	AAK76111	zebrafish sonic he
307	16	1.4	1256	22	AAK28450	Nucleotide sequenc
308	16	1.4	1256	22	AAK09033	zebrafish sonic he
309	16	1.4	1256	22	AAK10150	zebrafish sonic he
310	16	1.4	1256	22	AAK87078	Nucleotide sequenc
311	16	1.4	1256	22	AAK27017	zebrafish Sonic he
312	16	1.4	1256	24	AAK23803	zebrafish Sonic he
313	16	1.4	1260	13	AAK21976	Hybrid mini-vitel
314	16	1.4	1290	13	AAK21977	Hybrid mini-vitel
315	16	1.4	1290	13	AAK21980	Hybrid mini-vitel
316	16	1.4	1290	13	AAK21981	Hybrid mini-vitel
317	16	1.4	1317	22	AAK53387	S. epidermidis ope
318	16	1.4	1329	21	AAK71179	Human ORFX ORF2734
319	16	1.4	1334	21	AAK15805	Human prostate can
320	16	1.4	1335	22	AAK52115	Human AFP protein
321	16	1.4	1349	22	AAK199526	Human polynucleoti
322	16	1.4	1374	23	AAK73577	DNA encoding novel
323	16	1.4	1383	22	AAK66506	C. glutamicum codin
324	16	1.4	1393	7	AAK60225	Sequence of autono
325	16	1.4	1405	14	AAK46125	PE2 receptor (EP3
326	16	1.4	1432	22	AAK94247	Human full-length
327	16	1.4	1444	22	AAK44073	Oryza sativa perox
328	16	1.4	1455	21	AAK15005	CDNA encoding a hu
329	16	1.4	1460	21	AAK29840	RAB6c coding sequ
330	16	1.4	1461	23	ABK18553	Drosophila melanog
331	16	1.4	1506	23	ABK05251	H. pylori secreted
332	16	1.4	1509	18	AAV24861	H. pylori secreted
333	16	1.4	1509	18	AAV24959	Human WAVE3 CDNA
334	16	1.4	1509	22	AAK84403	DNA encoding novel
335	16	1.4	1523	22	AAK22913	DNA encoding novel
336	16	1.4	1525	22	AAK22912	DNA encoding novel
337	16	1.4	1583	24	ABK03464	Human DNA mismatch
338	16	1.4	1590	23	AAK39365	DNA encoding novel
339	16	1.4	1591	21	AAK33449	Arabidopsis thalia
340	16	1.4	1620	23	AAK70699	DNA encoding novel
341	16	1.4	1620	23	AAK90727	DNA encoding novel
342	16	1.4	1622	23	AAK87607	DNA encoding novel
343	16	1.4	1625	22	AAK199513	Human polynucleoti
344	16	1.4	1630	19	AAK14097	H. pylori GHP0 137
345	16	1.4	1638	21	AAK51437	Arabidopsis thalia
346	16	1.4	1644	22	AAK22750	Human cDNA encodin
347	16	1.4	1660	21	AAK65008	Membrane-bound pro
348	16	1.4	1660	22	AAK45998	Human DNA encoding
349	16	1.4	1660	22	AAK92073	Human PRO1115 CDNA
350	16	1.4	1660	22	AAK44154	Human PRO1115 CDNA
351	16	1.4	1710	22	AAK61026	P. putida RT2440-a
352	16	1.4	1713	17	AAK36389	Arlyl Beta-N-acetyl
353	16	1.4	1713	21	AAK38242	Vibrio furnissii e
354	16	1.4	1724	21	AAK15819	Human prostate can
355	16	1.4	1726	22	AAK52254	Human cDNA encodin
356	16	1.4	1755	22	AAK89200	Novel human membra
357	16	1.4	1758	22	AAK89199	Novel human membra
358	16	1.4	1764	23	AAK59058	DNA encoding novel
359	16	1.4	1770	21	AAK51279	Arabidopsis thalia
360	16	1.4	1773	23	AAK90107	DNA encoding novel
361	16	1.4	1794	23	AAK70895	DNA encoding novel
362	16	1.4	1794	23	AAK91006	DNA encoding novel
363	16	1.4	1887	22	AAK18090	Human cDNA sequenc
364	16	1.4	1893	24	AAK52571	CDNA sequence #358
365	16	1.4	1967	23	ABK07527	Drosophila melanog
366	16	1.4	1968	22	AAK21325	Human cDNA sequenc
367	16	1.4	2065	22	AAK72219	Human neovasculari
368	16	1.4	2095	23	ABK13403	Drosophila melanog
369	16	1.4	2107	14	AAK46124	PE2 receptor (EP3
370	16	1.4	2158	12	AAK14624	Plasmid pPATDP in
371	16	1.4	2158	17	AAK14372	Plasmid pPATDP (A
372	16	1.4	2158	20	AAK23229	Rat dunce-like pho
373	16	1.4	2158	21	AAK88164	Plasmid pPATDP 2.
374	16	1.4	2161	20	AAK57464	Rat U3 gene trap d

c 375	16	1.4	2173	19	AAV31987	Mouse Down syndrom	448	16	1.4	3452	22	AAK75977	Human immune/haema
c 376	16	1.4	2181	21	AAZ95576	CDNA encoding a hu	449	16	1.4	3504	22	AAK52083	Human polynucleoti
c 377	16	1.4	2182	24	AAZ59599	DNA encoding human	c 450	16	1.4	3506	22	ABL05250	Drosophila melanog
c 378	16	1.4	2192	23	AAST1438	DNA encoding novel	c 451	16	1.4	3592	23	AA584689	DNA encoding novel
c 379	16	1.4	2213	24	AA599922	Polynucleotide enc	c 452	16	1.4	3720	22	AAK53057	Human polynucleoti
c 380	16	1.4	2223	13	AAQ29187	CDNA encoding Plas	c 453	16	1.4	3734	22	AA572406	DNA encoding novel
c 381	16	1.4	2223	16	AAQ80908	Plasmodium falcipa	c 454	16	1.4	3763	19	AAV58194	Human myosin I-cha
c 382	16	1.4	2255	21	AAQ65614	Human ORFX ORF2069	c 455	16	1.4	3763	19	AA569872	DNA encoding novel
c 383	16	1.4	2274	16	AAQ75959	C. albicans caaur1	c 456	16	1.4	3787	22	AAH81775	Human differential
c 384	16	1.4	2274	17	AAAT10501	Aureobasidin sensi	c 457	16	1.4	3826	22	AAH54225	S. epidermidis gen
c 385	16	1.4	2288	23	ABL21072	Drosophila melanog	c 458	16	1.4	3891	23	ABL24402	Drosophila melanog
c 386	16	1.4	2322	22	AA526272	Human CDNA encodin	c 459	16	1.4	3967	23	ABL07526	Drosophila melanog
c 387	16	1.4	2340	20	AAH80866	DNA encoding human	c 460	16	1.4	3982	23	ABL23044	Drosophila melanog
c 388	16	1.4	2354	21	AAZ50348	Human secreted pro	c 461	16	1.4	4010	22	ABL18552	Drosophila melanog
c 389	16	1.4	2393	21	AAZ46135	CDNA encoding an a	c 462	16	1.4	4265	22	AAK52361	Human polynucleoti
c 390	16	1.4	2433	22	AD099336	Rat PRPDE90 CDNA e	c 463	16	1.4	4295	22	AA158456	Human polynucleoti
c 391	16	1.4	2450	23	ABL25910	Drosophila melanog	c 464	16	1.4	4351	17	AA156642	Coturnix sp. aroma
c 392	16	1.4	2456	12	AAO13362	Gene encoding poly	c 465	16	1.4	4379	22	AAK53395	Human polynucleoti
c 393	16	1.4	2540	22	AAH14650	Human CDNA sequenc	c 466	16	1.4	4379	22	AA160242	Human polynucleoti
c 394	16	1.4	2555	8	AAH70548	2.6 kbp fragment o	c 467	16	1.4	4409	21	AAV65585	Nucleotide sequenc
c 395	16	1.4	2565	23	AA585127	Varicella-zoster v	c 468	16	1.4	4409	22	AAAD10226	Pichia methanolica
c 396	16	1.4	2607	13	AAQ24233	DNA encoding novel	c 469	16	1.4	4409	22	AA55407	Nucleotide sequenc
c 397	16	1.4	2619	23	AA571968	DNA encoding novel	c 470	16	1.4	4409	22	AAAD02412	Pichia methanolica
c 398	16	1.4	2632	23	ABU04241	Drosophila melanog	c 471	16	1.4	4425	18	AAAT72781	Human interleukin-
c 399	16	1.4	2639	21	AAZ93040	Sequence encoding	c 472	16	1.4	4448	23	ABL14412	Drosophila melanog
c 400	16	1.4	2646	15	AAQ61607	Mutated GAL4 gene	c 473	16	1.4	4480	20	AAAX13257	Enterococcus faeca
c 401	16	1.4	2647	22	AD099339	Rat PRPDE92 CDNA e	c 474	16	1.4	4534	20	AAAX3042	Human IL-1ra BAC c
c 402	16	1.4	2678	23	ABU10806	Drosophila melanog	c 475	16	1.4	4539	22	ABA07240	Human pancreatic c
c 403	16	1.4	2679	23	AA594559	DNA encoding novel	c 476	16	1.4	4539	22	AAK89881	Human digestive sy
c 404	16	1.4	2701	24	ABU34325	Human Immune syste	c 477	16	1.4	4600	23	ABL18056	Drosophila melanog
c 405	16	1.4	2753	22	AAH14335	Human CDNA sequenc	c 478	16	1.4	4647	23	ABL07574	Drosophila melanog
c 406	16	1.4	2763	21	AAZ65286	Human secreted pro	c 479	16	1.4	4692	23	ABL13402	Drosophila melanog
c 407	16	1.4	2805	22	AA563223	Human full-length	c 480	16	1.4	4702	23	ABL10820	Drosophila melanog
c 408	16	1.4	2832	23	ABU04243	Drosophila melanog	c 481	16	1.4	4708	22	AAH18684	Human CDNA sequenc
c 409	16	1.4	2915	22	AA511662	Human CYP2B6 DNA 5	c 482	16	1.4	4767	21	AAAT71571	S. aggregatum PKS
c 410	16	1.4	2947	16	AAH87269	Human MSH2 gene.	c 483	16	1.4	4968	20	AAK20597	Polynucleotide seq
c 411	16	1.4	2950	22	AAH17486	Human CDNA sequenc	c 484	16	1.4	4980	22	AAAD16236	Mouse ATP-binding
c 412	16	1.4	3022	22	ABU09338	Rat PRPDE9 CDNA e	c 485	16	1.4	5017	23	AA592693	DNA encoding novel
c 413	16	1.4	3051	23	ABU23607	Drosophila melanog	c 486	16	1.4	5047	23	AA578835	DNA encoding novel
c 414	16	1.4	3095	16	AA593911	Human mismatch rep	c 487	16	1.4	5433	22	AAH99527	Human protein enco
c 415	16	1.4	3099	23	AA553411	Haemophilus influe	c 488	16	1.4	5541	23	ABL18092	Drosophila melanog
c 416	16	1.4	3109	16	AAQ93901	Human MSH2 gene, h	c 489	16	1.4	5767	23	ABL14646	Drosophila melanog
c 417	16	1.4	3118	21	AAAT15989	Human prostate can	c 490	16	1.4	6048	19	AAV09029	Human hml sodium c
c 418	16	1.4	3130	22	AA571971	DNA encoding novel	c 491	16	1.4	6048	22	AAAF30825	Human SCNA gene.
c 419	16	1.4	3133	22	AD099340	Rat PRPDE74 CDNA e	c 492	16	1.4	6053	22	AA546338	Tumour suppressor
c 420	16	1.4	3145	22	AAH75043	Nucleotide sequenc	c 493	16	1.4	6074	23	ABL066380	Drosophila melanog
c 421	16	1.4	3145	22	AAH76366	Human MSH2 CDNA.	c 494	16	1.4	6117	24	ABU34491	Human metastasis a
c 422	16	1.4	3148	22	AAH54685	S. epidermidis gen	c 495	16	1.4	6120	23	ABU01860	Drosophila melanog
c 423	16	1.4	3157	23	AA573521	DNA encoding novel	c 496	16	1.4	6200	22	AA546442	Tumour suppressor
c 424	16	1.4	3175	23	AA594564	DNA encoding novel	c 497	16	1.4	6259	24	ABL32290	Human immune syste
c 425	16	1.4	3182	21	AA588611	Human PRO1250 prot	c 498	16	1.4	6326	24	ADL22338	Chemically treated
c 426	16	1.4	3195	23	AA587692	DNA encoding novel	c 499	16	1.4	6664	24	AA561368	Human gene regulat
c 427	16	1.4	3209	14	AAQ34779	Marck's Disease VI	c 500	16	1.4	6911	17	AAAT34177	Corynebform sucrose
c 428	16	1.4	3269	23	ABU21122	Drosophila melanog	c 501	16	1.4	7090	23	ABL12034	Drosophila melanog
c 429	16	1.4	3286	22	AAH54271	S. epidermidis gen	c 502	16	1.4	7238	24	ABL32448	Human immune syste
c 430	16	1.4	3296	21	AAH76408	Human ORFX ORF1963	c 503	16	1.4	7259	23	ABL27520	Drosophila melanog
c 431	16	1.4	3301	22	AAZ51259	Human RNA-associat	c 504	16	1.4	7306	24	ABL33636	Human immune syste
c 432	16	1.4	3301	22	AAZ51282	Secreted protein g	c 505	16	1.4	7488	24	ABL33113	Human immune syste
c 433	16	1.4	3316	21	AAZ37047	Human PRO1250 (UNQ	c 506	16	1.4	7626	22	AA540044	Genomic sequence #
c 434	16	1.4	3316	22	AA521482	Human CDNA sequenc	c 507	16	1.4	7626	22	AA540044	Genomic sequence #
c 435	16	1.4	3316	22	AA542461	DNA encoding prote	c 508	16	1.4	7626	22	AA542461	Genomic sequence #
c 436	16	1.4	3317	22	AA560002	Human synthetase #	c 509	16	1.4	7831	22	ABA19111	Human nervous syst
c 437	16	1.4	3351	22	AA164331	Human transposase	c 510	16	1.4	7980	19	AAV44243	Lettuce resistance
c 438	16	1.4	3355	20	AAAX36342	Human TIE ligand N	c 511	16	1.4	8530	22	AA531089	Human diagnostic a
c 439	16	1.4	3355	21	AAAT77529	Human PRO188 CDNA	c 512	16	1.4	8639	20	AAK02895	Human IL-1ra BAC c
c 440	16	1.4	3355	21	AA521382	Human CDNA sequenc	c 513	16	1.4	8777	23	ABL23606	Drosophila melanog
c 441	16	1.4	3355	22	AA521382	Human anglogenesis	c 514	16	1.4	8876	24	ABL34076	Human immune syste
c 442	16	1.4	3364	22	AA521382	Human anglogenesis	c 515	16	1.4	9021	22	AA546326	Human immune syste
c 443	16	1.4	3384	22	AA521382	Drosophila melanog	c 516	16	1.4	9129	22	AA532754	Human genomic DNA
c 444	16	1.4	3413	22	AA550605	S. epidermidis gen	c 517	16	1.4	9134	22	AA532754	Human genomic DNA
c 445	16	1.4	3427	22	AA550605	S. epidermidis gen	c 518	16	1.4	9151	22	ABA14677	Human nervous syst
c 446	16	1.4	3442	22	AA554298	S. epidermidis gen	c 519	16	1.4	9153	22	ABA14676	Human nervous syst
c 447	16	1.4	3449	21	AA598215	Human colon cancer	c 520	16	1.4	9254	22	AA545381	Chemically pretrea

C 521	16	1.4	9254	22	AAS46392	Tumour suppressor
C 522	16	1.4	9295	23	ABL06144	Drosophila melanog
C 523	16	1.4	9295	23	ABL07236	Drosophila melanog
C 524	16	1.4	9964	24	ABL32099	Human immune syste
C 525	16	1.4	10078	22	AAS40045	Genomic sequence #
C 526	16	1.4	10078	22	AAK91462	Human digestive sy
C 527	16	1.4	10088	22	AAK5072	Human immune/haema
C 528	16	1.4	10169	14	AAO53522	Cellulose synthase
C 529	16	1.4	10191	23	ABL04240	Drosophila melanog
C 530	16	1.4	10283	23	ABL04242	Drosophila melanog
C 531	16	1.4	10655	23	ABL15398	Drosophila melanog
C 532	16	1.4	10929	22	AAS32755	Human genomic DNA
C 533	16	1.4	11172	22	AAH41168	Murine oligonucleo
C 534	16	1.4	11206	21	AAZ47807	Vector for trippin
C 535	16	1.4	11376	23	ABLI1258	Drosophila melanog
C 536	16	1.4	11710	24	AAH43718	E. coli genome sec
C 537	16	1.4	11711	22	ABA18962	Human nervous syst
C 538	16	1.4	11713	22	ABA18963	Human nervous syst
C 539	16	1.4	11881	22	AAS36624	Human cardiovascular
C 540	16	1.4	11881	22	AAS27691	DNA encoding novel
C 541	16	1.4	11881	22	AAS27693	DNA encoding novel
C 542	16	1.4	12831	22	AAK70373	Human immune/haema
C 543	16	1.4	13036	23	ABL10282	Drosophila melanog
C 544	16	1.4	13154	20	AAK13275	Enterococcus faeca
C 545	16	1.4	13537	22	AAK68964	Human immune/haema
C 546	16	1.4	13574	21	AAK81529	N. meningitidis pa
C 547	16	1.4	13865	20	AAK13137	Enterococcus faeca
C 548	16	1.4	13982	22	AAK65456	Human immune/haema
C 549	16	1.4	13982	22	AAK77762	Human immune/haema
C 550	16	1.4	13982	22	AAK84032	Human immune/haema
C 551	16	1.4	14904	22	AAK75386	Human immune/haema
C 552	16	1.4	15090	22	AAK72319	Human immune/haema
C 553	16	1.4	15254	22	AAK83135	Human immune/haema
C 554	16	1.4	15254	22	AAK83137	Human immune/haema
C 555	16	1.4	15255	22	AAK83136	Human immune/haema
C 556	16	1.4	15256	22	AAK83134	Human immune/haema
C 557	16	1.4	15366	22	AAS28623	Genomic sequence #
C 558	16	1.4	16159	22	ABA18491	Human nervous syst
C 559	16	1.4	16423	22	AAAD16645	Human novel protei
C 560	16	1.4	16423	22	AAS30242	DNA encoding rena
C 561	16	1.4	16748	22	AAK65193	Human immune/haema
C 562	16	1.4	16842	22	AAS46412	Tumour suppressor
C 563	16	1.4	16842	22	AAK61336	Human gene regulat
C 564	16	1.4	16870	20	AAK13035	Enterococcus faeca
C 565	16	1.4	17934	24	ABL93319	Human immune syste
C 566	16	1.4	18085	23	ABL09930	Drosophila melanog
C 567	16	1.4	18385	22	AAS28584	Genomic sequence #
C 568	16	1.4	18385	22	AAK79804	Human immune/haema
C 569	16	1.4	18786	23	AAS59579	Protonibacterium
C 570	16	1.4	19231	21	AAAB1470	N. meningitidis pa
C 571	16	1.4	19619	22	AAK28527	Genomic fragment #
C 572	16	1.4	20645	22	AAI05355	Human reproductive
C 573	16	1.4	20978	23	ABL20786	Drosophila melanog
C 574	16	1.4	21835	22	AAK66483	Human immune/haema
C 575	16	1.4	21913	22	AAI03377	Human reproductive
C 576	16	1.4	21913	22	AAI03378	Human reproductive
C 577	16	1.4	21913	22	AAI03379	Human reproductive
C 578	16	1.4	23075	22	ABA19112	Human nervous syst
C 579	16	1.4	24417	18	AAK97221	Pseudomonas aerugi
C 580	16	1.4	26006	22	AAI99233	Human excretory re
C 581	16	1.4	26006	22	AAS36463	Human cardiovascular
C 582	16	1.4	26006	22	AAI03357	Human reproductive
C 583	16	1.4	26006	22	AAS26664	Human genomic DNA
C 584	16	1.4	26006	22	AAI62592	Human breast or ov
C 585	16	1.4	26006	22	AAI63583	Human kidney relat
C 586	16	1.4	26013	22	AAI99231	Human excretory re
C 587	16	1.4	26013	22	AAS36461	Human cardiovascular
C 588	16	1.4	26013	22	AAI03355	Human reproductive
C 589	16	1.4	26013	22	AAS26662	Human genomic DNA
C 590	16	1.4	26013	22	AAI62590	Human breast or ov
C 591	16	1.4	26013	22	AAI63581	Human kidney relat
C 592	16	1.4	26018	22	AAI99232	Human excretory re
C 593	16	1.4	26018	22	AAS36462	Human cardiovascular
C 594	16	1.4	26018	22	AAI03596	Human reproductive
C 595	16	1.4	26018	22	AAS26663	Human genomic DNA
C 596	16	1.4	26018	22	AAI62591	Human breast or ov
C 597	16	1.4	26018	22	AAI63582	Human kidney relat
C 598	16	1.4	27579	22	AAK66484	Human immune/haema
C 599	16	1.4	32170	22	AAS28674	Genomic sequence #
C 600	16	1.4	32249	22	AAI04676	Human reproductive
C 601	16	1.4	36445	23	ABL18116	Drosophila melanog
C 602	16	1.4	36501	22	AAK64829	Human immune/haema
C 603	16	1.4	37337	23	AAS59518	Protonibacterium
C 604	16	1.4	49999	20	AAZ23901	Human LOBO homolog
C 605	16	1.4	50000	21	AAK6364	Polymorphic repeat
C 606	16	1.4	68750	21	AAZ55887	Sorangenin cellulose
C 607	16	1.4	69936	21	AAAB1479	N. meningitidis pa
C 608	16	1.4	71989	21	AAZ29349	Sorangenin cellulose
C 609	16	1.4	80251	23	ABL16442	Drosophila melanog
C 610	16	1.4	80251	23	ABL16443	Drosophila melanog
C 611	16	1.4	83390	21	AAK22283	BAC containing rep
C 612	16	1.4	90336	21	AAK22289	BAC containing rep
C 613	16	1.4	95223	21	AAK22282	BAC containing rep
C 614	16	1.4	99960	21	AAZ50905	Human TPC-1 partia
C 615	16	1.4	107820	22	AAAD16230	Human ATP-binding
C 616	16	1.4	124884	22	AAH74201	Nucleotide sequenc
C 617	16	1.4	125157	22	AAH74202	Nucleotide sequenc
C 618	16	1.4	172325	21	AAK21613	Neisseria meningit
C 619	16	1.4	335913	22	AAI61371	Soybean 240017 reg
C 620	16	1.4	335913	22	AAI61372	Soybean 240017 reg
C 621	16	1.4	349980	22	AAH64966	C glutaminc codin
C 622	16	1.4	349980	22	AAH68528	C glutaminc codin
C 623	16	1.4	465237	24	ABA90193	Human oestrogen re
C 624	16	1.4	611590	21	AAK22303	Arabidopsis thalia
C 625	16	1.4	611590	22	AAK95240	Human neuregulin-1
C 626	16	1.4	1503900	22	AAK96733	Human neuregulin-1
C 627	16	1.4	1664976	19	AAK21209	Methanococcus jan
C 628	16	1.4	1830121	17	AAK42063	Haemophilus influe
C 629	16	1.4	2944528	24	ABA03041	Listeria monocytog
C 630	16	1.3	19	21	AAK85195	Cyclin g1 ribozyme
C 631	16	1.3	19	21	AAK85196	Cyclin g1 ribozyme
C 632	16	1.3	19	22	AAH60357	Cyclin g1 ribozyme
C 633	16	1.3	19	22	AAH60358	Cyclin g1 ribozyme
C 634	16	1.3	23	21	AAK71038	Single nucleotide
C 635	16	1.3	23	21	AAK71077	Single nucleotide
C 636	16	1.3	23	21	AAK71089	Single nucleotide
C 637	16	1.3	23	21	AAK71110	Single nucleotide
C 638	16	1.3	29	20	AAV99736	Human secreted pro
C 639	16	1.3	30	22	AAAD12655	Human AHC2H01 CDN
C 640	16	1.3	30	22	AAK88740	Human catenin-bind
C 641	16	1.3	38	22	AAK86137	Human CHK1 ribozym
C 642	16	1.3	49	18	AAI80460	Hepatoma AS-30D Ty
C 643	16	1.3	51	22	AAI79445	Human silent SNP c
C 644	16	1.3	60	19	AAV49663	Primer (+8) for An
C 645	16	1.3	71	15	AAO77161	Human genome fragm
C 646	16	1.3	94	23	AAS50348	Staphylococcus aur
C 647	16	1.3	104	20	AAZ14021	Human gene express
C 648	16	1.3	118	22	ABA48167	Human foetal cell
C 649	16	1.3	118	22	ABA66044	Human foetal liver
C 650	16	1.3	118	22	ABA33127	Probe #11593 for g
C 651	16	1.3	118	22	AAK14467	Human brain expres
C 652	16	1.3	118	22	AAK40207	Human bone marrow
C 653	16	1.3	118	22	AAI20975	Probe #10908 for g
C 654	16	1.3	118	22	AAI16222	Probe #14908 used
C 655	16	1.3	118	22	AAI06688	Probe #6679 used t
C 656	16	1.3	140	22	AAK57447	Human immune/haema
C 657	16	1.3	141	22	ABA47816	Human breast cell
C 658	16	1.3	141	22	ABA65705	Human foetal liver
C 659	16	1.3	141	22	ABA65593	Human foetal liver
C 660	16	1.3	141	22	ABA52792	Probe #11258 for g
C 661	16	1.3	141	22	ABA33660	Probe #12126 for g
C 662	16	1.3	141	22	AAK14110	Human brain expres
C 663	16	1.3	141	22	AAK15020	Human brain expres
C 664	16	1.3	141	22	AAK39852	Human bone marrow
C 665	16	1.3	141	22	AAK40751	Human bone marrow
C 666	16	1.3	141	22	AAI20662	Probe #10595 for g

c 667	15	1.3	141	22	AA121514	Probe #11447 for g	c 740	15	1.3	380	14	AA059718	Human brain Express
c 668	15	1.3	141	22	AA145873	Probe #14559 used	c 741	15	1.3	380	22	AA527582	CDNA encoding nove
c 669	15	1.3	141	22	AA146806	Probe #15492 used	c 742	15	1.3	381	23	AA564398	DNA encoding novel
c 670	15	1.3	141	22	AA106362	Probe #6353 used t	c 743	15	1.3	383	21	AA667080	Pinus radiata cell
c 671	15	1.3	141	22	AA107210	Probe #7201 used t	c 744	15	1.3	383	22	ABA11395	Human nervous syst
c 672	15	1.3	148	22	ABA48694	Human breast cell	c 745	15	1.3	385	22	AA136640	Probe #5326 used t
c 673	15	1.3	148	22	AA121530	Probe #11463 for g	c 746	15	1.3	387	19	AAV44958	Anti-HIV-1 group O
c 674	15	1.3	148	22	AA107226	Probe #7217 used t	c 747	15	1.3	388	22	AA541553	CDNA encoding nove
c 675	15	1.3	159	17	AA131610	Klebsiella pneumonia	c 748	15	1.3	389	21	AAA98827	Human proliferatio
c 676	15	1.3	160	23	AA549197	Staphylococcus aur	c 749	15	1.3	389	21	AAA98108	Human proliferatio
c 677	15	1.3	165	18	AAV75450	Staphylococcus aur	c 750	15	1.3	389	22	AA125952	Human breast cance
c 678	15	1.3	160	22	AAH64969	C glutamylum codin	c 751	15	1.3	390	22	ABA45095	Human breast cell
c 679	15	1.3	191	21	AAAC12991	Human secreted pro	c 752	15	1.3	390	22	AAK03802	Human brain expres
c 680	15	1.3	195	22	AA126235	Human breast cance	c 753	15	1.3	390	22	AAK29269	Human bone marrow
c 681	15	1.3	199	22	AA119185	Human breast cance	c 754	15	1.3	390	22	AA133868	Probe #3801 for ge
c 682	15	1.3	216	17	AA131609	Klebsiella pneumonia	c 755	15	1.3	390	22	AA135229	Probe #3915 used t
c 683	15	1.3	217	21	AAAC16279	Human secreted pro	c 756	15	1.3	390	22	AA103772	Probe #3723 used t
c 684	15	1.3	226	11	AAO05051	Recombinant AatI g	c 757	15	1.3	392	22	AAH55612	Human breast tumor
c 685	15	1.3	250	23	AA549843	Staphylococcus aur	c 758	15	1.3	395	21	AAH87152	Rat hepatocyte car
c 686	15	1.3	250	23	AA549849	Staphylococcus aur	c 759	15	1.3	395	22	AA183339	Human polynucleoti
c 687	15	1.3	257	18	AAAT72461	Human CII-3 gene 1	c 760	15	1.3	396	23	AB124809	Drosophila melanog
c 688	15	1.3	262	16	AAAT23222	Human gene signatu	c 761	15	1.3	397	22	AAAF65942	Novel human polynu
c 689	15	1.3	262	21	AAAC24397	Human secreted pro	c 762	15	1.3	399	22	ABA54022	Human foetal liver
c 690	15	1.3	263	19	AAV03373	2-Oxo-glutarate de	c 763	15	1.3	399	22	ABA23776	Probe #2242 for ge
c 691	15	1.3	268	21	AAAT70684	Human alpha-Gal A	c 764	15	1.3	399	22	AAK02295	Human brain expres
c 692	15	1.3	268	21	AAA75433	5' end of cDNA of	c 765	15	1.3	399	22	AAK27739	Human bone marrow
c 693	15	1.3	287	13	AAO26399	PCIB4223. Synthet	c 766	15	1.3	399	22	AA112313	Probe #2252 for ge
c 694	15	1.3	289	20	AAV88814	EST clone HO1216.	c 767	15	1.3	399	22	AA133675	Probe #2361 used t
c 695	15	1.3	284	20	AAAT41499	Human secreted pro	c 768	15	1.3	399	22	AA102223	Probe #2224 used t
c 696	15	1.3	287	21	AAAC04510	Human secreted pro	c 769	15	1.3	401	21	AAAT80677	Human colon cancer
c 697	15	1.3	288	22	AA135287	Human musculoskele	c 770	15	1.3	401	22	AAK96571	Human neurogulin g
c 698	15	1.3	300	20	AAAT41557	Human gene express	c 771	15	1.3	401	22	AAK96573	Human neurogulin g
c 699	15	1.3	300	20	AAAT41557	Human gene express	c 772	15	1.3	401	22	AAK98064	Human neurogulin g
c 700	15	1.3	303	20	AAV89591	EST clone CN951.	c 773	15	1.3	401	22	AAK98066	Human neurogulin g
c 701	15	1.3	308	22	AA136581	Human musculoskele	c 774	15	1.3	402	14	AAO37826	Sequence of the pa
c 702	15	1.3	309	22	AA190840	Human polynucleoti	c 775	15	1.3	403	22	AAAF67382	Novel human polynu
c 703	15	1.3	310	20	AAAT40636	Human secreted pro	c 776	15	1.3	403	15	AAAF67382	Sequence of VHH DN
c 704	15	1.3	310	22	AAAT4510	Human breast cance	c 777	15	1.3	405	22	ABA08492	Human taste recept
c 705	15	1.3	312	21	AAAC04313	Human secreted pro	c 778	15	1.3	410	23	AB103565	Drosophila melanog
c 706	15	1.3	315	22	AAAL35120	Human musculoskele	c 779	15	1.3	415	20	AAAT06971	Zs199 expressed se
c 707	15	1.3	315	22	AAAL00773	Human reproductiv	c 780	15	1.3	415	21	AAAT08285	Expressed Sequence
c 708	15	1.3	320	20	AAAT98198	Nucleotide sequenc	c 781	15	1.3	415	22	AAAT27352	CDNA encoding nove
c 709	15	1.3	322	22	AAAT39155	Novel human diagno	c 782	15	1.3	416	21	AAAC24897	Human secreted pro
c 710	15	1.3	327	21	AAAT51986	Salmonella Pathoge	c 783	15	1.3	418	22	AAAT24817	DNA encoding novel
c 711	15	1.3	327	22	AAAT87158	Human immune/haema	c 784	15	1.3	421	21	AAAC92324	ADP-ribosylation f
c 712	15	1.3	330	20	AAAT41237	Human secreted pro	c 785	15	1.3	421	22	AAAC32214	Human secreted pro
c 713	15	1.3	332	22	AAAT75299	Human foetal liver	c 786	15	1.3	421	22	ABA571332	Human foetal liver
c 714	15	1.3	332	22	ABA33952	Probe #18418 for g	c 787	15	1.3	425	22	AAH11765	Human CDNA clone (
c 715	15	1.3	332	22	AAAT39159	Novel human diagno	c 788	15	1.3	426	22	AAAT54082	Murine transcripti
c 716	15	1.3	332	22	AAAT3852	Human brain expres	c 789	15	1.3	427	22	AAAT67464	Novel human polynu
c 717	15	1.3	332	22	AAAT49933	Human bone marrow	c 790	15	1.3	430	22	ABA88798	Escherichia coli p
c 718	15	1.3	332	22	AAAT27030	Probe #16963 for g	c 791	15	1.3	431	22	AAAT08207	Human breast cance
c 719	15	1.3	332	22	AAAT55863	Probe #24549 used	c 792	15	1.3	433	22	AAAL12678	Human breast cance
c 720	15	1.3	334	21	AAAT29477	Human secreted pro	c 793	15	1.3	435	22	AAAT52461	S. epidermidis ope
c 721	15	1.3	339	23	AAAT89368	DNA encoding novel	c 794	15	1.3	441	20	AAAT83998	Conopeptide propop
c 722	15	1.3	347	21	AAAT71070	Single nucleotide	c 795	15	1.3	441	20	AAAT70369	Human immune/haema
c 723	15	1.3	347	21	AAAT71109	Single nucleotide	c 796	15	1.3	444	22	AAAT98964	Human excretory re
c 724	15	1.3	347	22	AAAT64288	Human immune/haema	c 797	15	1.3	444	22	AAAT63314	Human kidney relat
c 725	15	1.3	348	22	AAAT35958	Human cardiovascular	c 798	15	1.3	449	22	AAAT09347	Amplicon DNA compr
c 726	15	1.3	348	22	AAAT35959	Human cardiovascular	c 799	15	1.3	450	19	AAAT44959	Anti-HIV-1 group O
c 727	15	1.3	348	22	AAAT03578	Cynomolgus IAP-11k	c 800	15	1.3	450	22	ABA13305	Human nervous syst
c 728	15	1.3	351	22	AAAT03576	Baboon IAP-11k pr	c 801	15	1.3	452	22	ABA18305	Human nervous syst
c 729	15	1.3	351	22	AAAT03579	Gorilla IAP-11k pr	c 802	15	1.3	455	22	ABA42688	Human breast cell
c 730	15	1.3	351	22	AAAT03580	Rhesus IAP-11k pr	c 803	15	1.3	455	22	ABA53112	Human foetal liver
c 731	15	1.3	352	22	AAAT86079	Human polynucleoti	c 804	15	1.3	455	22	ABA22886	Probe #1352 for ge
c 732	15	1.3	362	21	AAAT26554	Human secreted pro	c 805	15	1.3	455	22	AAAT01362	Human brain expres
c 733	15	1.3	365	21	AAAT71040	Single nucleotide	c 806	15	1.3	455	22	AAAT26818	Human bone marrow
c 734	15	1.3	365	21	AAAT71079	Single nucleotide	c 807	15	1.3	455	22	AAAT11448	Probe #1381 for ge
c 735	15	1.3	365	21	AAAT71091	Single nucleotide	c 808	15	1.3	455	22	AAAT32719	Probe #1405 used t
c 736	15	1.3	365	21	AAAT71112	Single nucleotide	c 809	15	1.3	455	22	AAAT01365	Probe #1356 used t
c 737	15	1.3	366	22	AAAT01254	Human Erbin probe	c 810	15	1.3	456	21	AAAT59434	Nucleotide sequenc
c 738	15	1.3	367	23	AAAT92301	DNA encoding novel	c 811	15	1.3	461	22	AAAT19117	Human breast cance
c 739	15	1.3	369	22	AAAT93990	Human foetal cDNA,	c 812	15	1.3	465	23	AAAT564971	DNA encoding novel

813	15	1.3	466	22	ABA56596	Human foetal liver
814	15	1.3	471	22	ABA43040	Human breast cell
815	15	1.3	471	22	ABA53454	Human foetal liver
816	15	1.3	471	22	ABA23225	Probe #1691 for ge
817	15	1.3	471	22	AAK01724	Human brain expres
818	15	1.3	471	22	AAK27177	Human bone marrow
819	15	1.3	471	22	AAI11763	Probe #1696 for ge
820	15	1.3	471	22	AAI33073	Probe #1759 used t
821	15	1.3	471	22	AAI01692	Probe #1683 used t
822	15	1.3	472	22	ABA59318	Human foetal liver
823	15	1.3	472	22	AAK07536	Human brain expres
824	15	1.3	472	22	AAK33332	Human bone marrow
825	15	1.3	472	22	AAI33119	Probe #7805 used t
826	15	1.3	473	22	AAK57817	Human immune/haema
827	15	1.3	474	18	AAAT67779	H. pylori membrane
828	15	1.3	474	18	AAAT77459	H. pylori transmem
829	15	1.3	474	22	AAAS09369	Amplicon DNA compr
830	15	1.3	475	21	AAAS6026	Human chromosome 1
831	15	1.3	475	22	AAK63082	Human immune/haema
832	15	1.3	480	21	AAAC00962	Human secreted pro
833	15	1.3	485	21	AAAB6871	EST clone BK200.
834	15	1.3	485	21	AAAB82372	N. meningitidis pa
835	15	1.3	489	20	AAAX98196	Nucleotide sequenc
836	15	1.3	489	22	ABA33584	Human breast cell
837	15	1.3	489	22	AAI12335	Probe #2268 for ge
838	15	1.3	489	22	AAI02249	Probe #2240 used t
839	15	1.3	492	21	AAZ53095	Neisseria gonorrhoe
840	15	1.3	496	22	AAK58660	Human immune/haema
841	15	1.3	500	21	AAAC3588	Cat flea head and
842	15	1.3	501	23	AAAS53711	Helicobacter pylori
843	15	1.3	501	24	AAAS61795	Lung small cell ca
844	15	1.3	509	19	AAAI4418	H. pylori GHPD 693
845	15	1.3	510	16	AAAG2884	Human CTLA-8 cDNA.
846	15	1.3	510	24	AAAT77244	Human cytokine-lik
847	15	1.3	514	21	AAAC78252	Human cancer assoc
848	15	1.3	514	22	AAAB64923	Human secreted pro
849	15	1.3	517	22	ABA63078	Human foetal liver
850	15	1.3	517	22	ABA30333	Probe #8799 for ge
851	15	1.3	517	22	AAAI1502	Human brain expres
852	15	1.3	517	22	AAK37280	Human bone marrow
853	15	1.3	517	22	AAI18109	Probe #8042 for ge
854	15	1.3	517	22	AAI43113	Probe #11799 used
855	15	1.3	519	22	ABA60843	Human foetal liver
856	15	1.3	519	22	ABA28850	Probe #7316 for ge
857	15	1.3	519	22	AAK09130	Human brain expres
858	15	1.3	519	22	AAK35019	Human bone marrow
859	15	1.3	519	22	AAI40736	Probe #9422 used t
860	15	1.3	536	21	AAAB68132	Pinus radiata flav
861	15	1.3	537	17	AAAT31608	Klebsiella pneumon
862	15	1.3	546	21	AAZ38326	Human transmembran
863	15	1.3	555	21	AAAC41592	Arabidopsis thalia
864	15	1.3	555	22	AAH09178	Human cDNA clone (
865	15	1.3	561	23	ABLT27217	Drosophila melanog
866	15	1.3	563	22	AAK73488	Human immune/haema
867	15	1.3	563	22	AAK80627	Human immune/haema
868	15	1.3	564	24	ABK09691	Human ovarian tumo
869	15	1.3	565	18	AAAF10630	Fusarium venenatum
870	15	1.3	567	21	AAAF13869	Gene coding for L-
871	15	1.3	567	21	AAAF08472	Fusarium venenatum
872	15	1.3	572	19	AAH08763	Human cDNA clone (
873	15	1.3	572	19	AAAI4458	H. pylori GHPD 951
874	15	1.3	574	22	ABA60564	Human foetal liver
875	15	1.3	574	22	ABA28708	Probe #7174 for ge
876	15	1.3	574	22	AAK08846	Human brain expres
877	15	1.3	574	22	AAK34734	Human bone marrow
878	15	1.3	574	22	AAI16821	Probe #6754 for ge
879	15	1.3	577	22	AAI10453	Probe #9139 used t
880	15	1.3	577	22	AAI15785	Human breast cance
881	15	1.3	579	22	AAK11759	Human brain expres
882	15	1.3	579	23	AAH09463	Human cDNA clone (
883	15	1.3	580	23	AAAS70599	DNA encoding novel
884	15	1.3	580	23	AAAS7180	DNA encoding novel
885	15	1.3	594	22	AAAS02054	DNA encoding molec
886	15	1.3	595	22	ABA06665	Human cDNA SEQ ID
887	15	1.3	595	22	AAAS28835	Human immunoglobul
888	15	1.3	596	22	ABA62787	Human foetal liver
889	15	1.3	596	22	ABA30080	Probe #8546 for ge
890	15	1.3	596	22	AAK11185	Human brain expres
891	15	1.3	596	22	AAK36992	Human bone marrow
892	15	1.3	596	22	AAI17834	Probe #1767 for ge
893	15	1.3	596	22	AAI42804	Probe #11490 used
894	15	1.3	598	22	ABA63325	Human foetal liver
895	15	1.3	598	22	AAI18329	Probe #8262 for ge
896	15	1.3	607	17	AAAT68893	Haemophilus influe
897	15	1.3	607	22	AAK83921	Human immune/haema
898	15	1.3	608	22	AAAS41002	cDNA encoding nove
899	15	1.3	612	22	AAH31452	Human olfactory re
900	15	1.3	614	22	AAH31450	Human olfactory re
901	15	1.3	618	22	AAK78164	Human immune/haema
902	15	1.3	618	22	AAK78165	Human immune/haema
903	15	1.3	618	22	AAK78166	Human immune/haema
904	15	1.3	622	19	AAAT98746	DNA encoding a S.
905	15	1.3	622	22	AAH31454	Human olfactory re
906	15	1.3	628	22	AAAF12979	Aspergillus oryzae
907	15	1.3	629	21	AAAF12979	Human olfactory re
908	15	1.3	632	22	AAH31453	Human immune/haema
909	15	1.3	634	22	AAK71202	Human immune/haema
910	15	1.3	635	18	AAAV74505	Staphylococcus aur
911	15	1.3	643	22	AAH07292	Human cDNA clone (
912	15	1.3	647	20	AAAX37381	Human secreted pro
913	15	1.3	649	20	AAAX97883	Human secreted pro
914	15	1.3	649	20	AAAX06968	Human secretory pe
915	15	1.3	649	21	AAZ08284	Human zsf19 gene.
916	15	1.3	651	19	AAAV19119	DNA encoding a Str
917	15	1.3	651	20	AAAX21557	S. pneumoniae M pr
918	15	1.3	653	22	AAAS56387	Human cDNA for an
919	15	1.3	653	23	AAAS49439	Staphylococcus aur
920	15	1.3	654	22	AAAL09113	Staphylococcus aur
921	15	1.3	657	21	AAAF07813	Human breast cance
922	15	1.3	663	22	ABA88116	Fusarium venenatum
923	15	1.3	667	22	ABA18844	Escherichia coli p
924	15	1.3	667	22	ABA18845	Human nervous syst
925	15	1.3	667	22	AAH29009	Drosophila melanog
926	15	1.3	669	22	AAAB68159	C glutamicum codin
927	15	1.3	677	18	AAAV5974	Staphylococcus aur
928	15	1.3	677	21	AAAC39805	Arabidopsis thalia
929	15	1.3	678	22	AAK92248	Human cDNA 5'-end
930	15	1.3	678	22	AAK93508	Human cDNA clone r
931	15	1.3	681	13	AAO29259	Human calcium chan
932	15	1.3	684	20	AAAL20377	Borrelia burgdorfe
933	15	1.3	689	22	AAAL24694	Human breast cance
934	15	1.3	695	22	AAAS59843	DNA encoding a tag
935	15	1.3	706	22	AAK87618	Human immune/haema
936	15	1.3	706	22	AAAB89239	Escherichia coli p
937	15	1.3	709	19	AAAV27371	Streptococcus pneu
938	15	1.3	711	18	AAAT67962	H. pylori transmem
939	15	1.3	712	21	AAAC36852	Arabidopsis thalia
940	15	1.3	714	20	AAAX97884	Human secreted pro
941	15	1.3	717	22	AAK87616	Human immune/haema
942	15	1.3	718	20	AAZ10655	Human immune/haema
943	15	1.3	719	23	ABLI19255	cDNA encoding a hu
944	15	1.3	720	14	AAO45918	Drosophila melanog
945	15	1.3	721	22	AAH04090	Phage PI ref gene.
946	15	1.3	722	22	AAK75721	Human cDNA clone (
947	15	1.3	723	22	AAK61799	Human immune/haema
948	15	1.3	726	23	AAAS73558	DNA encoding novel
949	15	1.3	729	22	AAAL36929	Human cDNA clone (
950	15	1.3	730	17	AAAT88425	K. pneumoniae dete
951	15	1.3	730	22	ABA76835	Klebsiella pneumon
952	15	1.3	733	22	AAK53226	Human polynucleoti
953	15	1.3	735	21	AAAF12207	Aspergillus oryzae
954	15	1.3	735	22	AAAL36929	Human musculoskele
955	15	1.3	735	22	AAAS2586	S. epidermidis ope
956	15	1.3	743	22	AAK59603	Human immune/haema
957	15	1.3	752	22	AAAL24658	Human breast cance
958	15	1.3	756	22	AAH03408	Human cDNA clone (

QY 721 tatttaacaacacggagcgttaagaagaactggttacgagccagccagatgcatctgcg 780
 Db 721 tatttaacaacacggagcgttaagaagaactggttacgagccagccagatgcatctgcg 780
 QY 781 ggtggtgccaactcactgatagaacaacccgtaagatgattacatggtgtgtgcag 840
 Db 781 ggtggtgccaactcactgatagaacaacccgtaagatgattacatggtgtgtgcag 840
 QY 841 acgttaactacacgagactctacagattctacccgtatgaaagaattatagactctac 900
 Db 841 acgttaactacacgagactctacagattctacccgtatgaaagaattatagactctac 900
 QY 901 gcatatctatgataaagaatgatacgtatgatacatatggtgctcaccctgattcccg 960
 Db 901 gcatatctatgataaagaatgatacgtatgatacatatggtgctcaccctgattcccg 960
 QY 961 tcacagccgttcacccgacgataaatacgtcgttaaatctatcgcgatttcgttaaa 1020
 Db 961 tcacagccgttcacccgacgataaatacgtcgttaaatctatcgcgatttcgttaaa 1020
 QY 1021 actgaaaaaacaactgataaatacgcgcagatggtttcgcctgtgtctctgtccacgcag 1080
 Db 1021 actgaaaaaacaactgataaatacgcgcagatggtttcgcctgtgtctctgtccacgcag 1080
 QY 1081 aacgcgcgcccaataatgataacgctgctgcatcactctgttgaagacctgcactaa 1137
 Db 1081 aacgcgcgcccaataatgataacgctgctgcatcactctgttgaagacctgcactaa 1137

RESULT 2

AAF60839 standard; DNA; 2122 BP.

AAF60839;

16-MAY-2001 (first entry)

Pseudomonas sp export system associated DNA ORF02378a.

Export system; transgenic plant; translocation; plant growth;

plant development; plant yield; soil quality; phytoprotection; ds.

Pseudomonas sp.

DE19935105-A1.

01-FEB-2001.

27-JUL-1999; 99DE-1035105.

27-JUL-1999; 99DE-1035105.

(TIGR-) TIGR INST GENOMIC RES.

(GEBB-) GEBB BIOTECHNOLOGISCHE FORSCHUNG MBH.

(DKFZ-) DKFZ DEUT KREBSFORSCHUNGSZENTRUM.

(MEDI-) MEDIZINISCHE HOCHSCHULE HANNOVER.

WPI: 2001-192471/20.

Claim 3a: Page 11-12; 26pp; German.

This invention describes novel DNA sequences (I) that express products having the biological function of export systems. The invention also describes (a) recombinant expression vectors containing (I); (b) prokaryotic and eukaryotic cells transformed or transfected with (I) or the vector of (a); (c) production of export systems by culturing cells of (b); (d) (partial) expression products (II) of (I), and synthetic proteins or peptides with the same sequences; (e) mono- or polyclonal antibodies (Ab) specific for (II); (f) hybridoma cells that produce

CC monoclonal Ab; and (g) transgenic plants that contain cells of (b). The
 CC export systems encoded by (I) translocate, through the bacterial cell
 CC wall, endogenous or modified metabolites or endogenously or
 CC heterologously expressed proteins. (I), and their fragments, are useful:
 CC (1) for expression of recombinant export systems; (2) as probes and
 CC primers for detection, isolation and amplification of full-length cDNA
 CC sequences; and (3) for producing transgenic plants. Cells transformed
 CC with (I), also recombinant export systems or synthetic peptides or
 CC proteins with the same activities, are used to promote growth,
 CC development and yield of plants, particularly leguminosae. Host cells
 CC that express export systems improve soil quality, are phytoprotective and
 CC improve development, growth and yield of plants.

SQ Sequence 2122 BP; 411 A; 696 C; 705 G; 309 T; 1 other;

Query Match 1.9%; Score 22; DB 22; Length 2122;
 Best Local Similarity 100.0%; Pred. No. 0.61;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 399 gctgctgagcctggcggtgag 420
 Db 2068 gctgctgagcctggcggtgag 2089

RESULT 3

ABL01346 standard; DNA; 746 BP.

ABL01346;

15-MAR-2002 (first entry)

Murine apoptosis related DNA sequence #11.

Apoptosis; mouse; cancer; autoimmune disease; viral infection;

Alzheimer's disease; Parkinson's disease; Huntington's disease;

reperfusion injury; stroke; liver damage; dilatory cardiomyopathy;

transgenic animal; hepatotropic; antialcoholism; cytostatic;

immunopressiveive; virucide; nootropic; neuroprotective; vasotropic;

antiparkinsonian; cerebroprotective; ds.

Mus sp.

DE10126344-A1.

24-JAN-2002.

30-MAY-2001; 2001DE-1026344.

14-JUL-2000; 2000DE-1034303.

(PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.

Grimm S, Schoenfeld N, Brazillis E, Cramer U, Gewies A, Voss F;

Mund T, Albayrak T, Gille H, Klein M;

WPI: 2002-115563/16.

Claim 1: Page 136; 227pp; German.

The present invention relates to nucleic acids from the mouse, where the
 CC nucleic acid is associated with apoptosis. The sequences associated with
 CC the diagnosis, treatment and prevention of diseases associated with
 CC excessive or inadequate apoptosis, including tumours, autoimmune
 CC diseases, viral infections, degenerative diseases (Alzheimer's,
 CC Parkinson's and Huntington's diseases), reperfusion injury, stroke and
 CC alcohol-induced injury to the liver, for identifying agents for treating
 CC these diseases, and to prepare transgenic animals in which expression of

CC an apoptosis related sequence is altered. These are useful for genetic
CC and/or pharmacological investigations of apoptosis and related diseases,
CC including dilatory cardiomyopathy. The present sequence is one of the
CC apoptosis related sequences of the invention.

XX
SQ Sequence 746 BP, 123 A; 220 C; 182 G; 201 T; 20 other;

Query Match 1.8%; Score 20; DB 24; Length 746;
Best Local Similarity 100.0%; Pred. No. 6.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 938 tgggcttcaccctgatgttc 957
|||||
Db 497 tgggcttcaccctgatgttc 516

RESULT 4

AAK61604 standard; cDNA; 882 BP.

XX AAK61604;

XX 06-NOV-2001 (first entry)

DE Human Immune/haematopoietic antigen encoding cDNA SEQ ID NO:6664.

XX Human; Immune; haematopoietic; Immune/haematopoietic antigen; Cancer;

KW cytostatic; gene therapy; vaccine; metastasis; ss.

XX Homo sapiens.

OS
PN WO200157182-A2.

XX
PD 09-AUG-2001.

XX
PF 17-JAN-2001; 2001WO-US01354.

XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
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Best Local Similarity 100.0%; Pred. No. 21;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 670 ttatgaaagaattacga 688

RESULT 6
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ID AAC40124 standard; DNA; 1289 BP.
XX
AC AAC40124;
XX
DT 17-OCT-2000 (first entry)
XX

DE Arabidopsis thaliana DNA fragment SEQ ID NO: 27143.
XX Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KM metabolic pathway; promoter; termination sequence; ss.
OS Arabidopsis thaliana.
XX EP1033405-A2.
XX
PD 06-SEP-2000.
XX
XX
XX 25-FEB-2000; 2000EP-0301439.
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XX 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
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Query Match 1.7%; Score 19; DB 21; Length 1289;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Caps 0;

OY 875 ttatgaaagaattatagca 893
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DB 670 ttatgaaagaattatagca 688

RESULT 7

AAV74939/c
ID AAV74939 standard; DNA: 453 BP.

AC AAV74939;

DT 16-MAR-1999 (first entry)

DE Staphylococcus aureus contig SEQ ID #628.

XX Computer readable medium; vaccine; S.aureus infection; immunodetection;
KW cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;
KW skin infection; surgical wound infection; scalded skin syndrome;
KW toxic shock syndrome; ds.

XX

OS Staphylococcus aureus.
XX
XX EP786519-A2.
XX
PD 30-JUL-1997.
XX
XX 07-JAN-1997; 97EP-0100117.
XX
XX 05-JAN-1996; 96US-0009861.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX Barash SC, Choi GH, Dillon PJ, Fannon MR, Kunsch CA;
PI Rosen CA;
XX
XX WPI; 1997-374922/35.
DR
XX
XX Polynucleotide(s) and proteins derived from Staphylococcus aureus -
PT stored on computer readable medium and used in the production of
PT anti-S.aureus vaccines

PS Claim 1; Page 1555; 3271pp; English.

XX This sequence represents one of 5191 Staphylococcus aureus DNA sequences
CC of the invention. The DNA sequences are recorded on a computer readable
CC medium, preferably selected from a floppy or hard disk, random access
CC memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using
CC the S.aureus DNA sequences allows putative functions to be assigned so
CC that protein-encoding or regulatory regions of commercial, therapeutic or
CC industrial importance can be obtained. Specifically, sequences which are
CC likely to encode antigens have been identified and these polypeptides can
CC be used in a vaccine composition against S.aureus infection. The
CC polypeptides can also be used in a kit for the immunodetection of
CC S.aureus in a sample. S.aureus is implicated in numerous human diseases,
CC including cellulitis, eyelid infections, food poisoning, osteomyelitis,
CC skin and surgical wound infections, scalded skin syndrome, toxic shock
CC syndrome, etc. Organisms transformed with the DNA sequences can be used
CC for recombinant production of the polypeptides. The new DNA sequences
CC (and their fragments) are useful as primers or probes for isolating
CC homologues of any of the S.aureus DNA sequences contained on the
CC computer readable medium.

XX Sequence 453 BP; 108 A; 82 C; 58 G; 202 T; 3 other;

Query Match 1.6%; Score 18; DB 18; Length 453;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 566 actctcttgatacatgacg 583
|||||
DB 178 ACTCTCTTGTGATCATACG 161

RESULT 8

ABA63976/c
ID ABA63976 standard; DNA: 581 BP.

AC ABA63976;

DT 01-FEB-2002 (first entry)

DE Human foetal liver single exon nucleic acid probe #12281.

XX Human; foetal liver; gene expression; single exon nucleic acid probe; ss.

OS Homo sapiens.

XX WO200157277-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US00669.

```
XX 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-483447/52.
XX
XX Human genome-derived single exon nucleic acid probes useful for
XX analyzing gene expression in human fetal liver -
XX
XX Claim 1; SEQ ID NO 12281; 639pp + sequence listing; English.
XX
XX The invention relates to a single exon nucleic acid probe for
XX measuring human gene expression in a sample derived from human foetal
XX liver. The single exon nucleic acid probes may be used for predicting,
XX measuring and displaying gene expression in samples derived from human
XX fetal liver. The present sequence is a single exon nucleic acid
XX probe of the invention.
XX Note: The sequence data for this patent did not form part of the
XX printed specification, but was obtained in electronic format directly
XX from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 581 BP; 115 A; 144 C; 201 G; 121 T; 0 other;
XX
XX
XX Query Match 1.6%; Score 18; DB 22; Length 581;
XX Best Local Similarity 100.0%; Pred. No. 68;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Oy 43 ctgtgctgctgctgtct 60
XX ||||||||||||||||
XX Db 168 CTGTGCTGCTGCTGCTCT 151
XX
XX RESULT 9
XX ABA31149/c
XX ID ABA31149 standard; DNA; 581 BP.
XX
XX AC ABA31149;
XX
XX DT 23-JAN-2002 (first entry)
XX
XX DE Probe #9615 for gene expression analysis in human heart cell sample.
XX
XX Human; gene expression; heart; microarray; vascular system; probe;
XX cardiovascular disease; hypertension; cardiac arrhythmia;
XX congenital heart disease; ss.
XX
XX Homo sapiens.
XX
XX MO200157274-A2.
XX
XX PD 09-AUG-2001.
XX
XX PF 30-JAN-2001; 2001WO-US00666.
XX
XX PR 04-FEB-2000; 2000US-0180312.
XX PR 26-MAY-2000; 2000US-0207456.
XX PR 30-JUN-2000; 2000US-0608408.
XX PR 03-AUG-2000; 2000US-0632366.
XX PR 21-SEP-2000; 2000US-0234687.
XX PR 27-SEP-2000; 2000US-0236359.
XX PR 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
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XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-488899/53.
XX
XX Single exon nucleic acid probes for analyzing gene expression in human
XX hearts -
XX
XX Claim 1; SEQ ID NO 9615; 530pp; English.
XX
XX The present invention relates to single exon nucleic acid probes for
XX measuring human gene expression in a sample derived from human heart. The
XX present sequence is one such probe. The probes may be used for
XX predicting, measuring and displaying gene expression in samples derived
XX from the human heart via microarrays. By measuring gene expression, the
XX probes are useful for predicting, diagnosing, grading, staging,
XX monitoring and prognosing diseases of the human heart and vascular system
XX e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
XX congenital heart disease.
XX Note: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 581 BP; 115 A; 144 C; 201 G; 121 T; 0 other;
XX
XX
XX Oy 43 ctgtgctgctgctgtct 60
XX ||||||||||||||||
XX Db 168 CTGTGCTGCTGCTGCTCT 151
XX
XX RESULT 10
XX AAK12475/c
XX ID AAK12475 standard; DNA; 581 BP.
XX
XX AC AAK12475;
XX
XX DT 05-NOV-2001 (first entry)
XX
XX DE Human brain expressed single exon probe SEQ ID NO: 12466.
XX
XX Human; brain expressed exon; gene expression analysis; probe;
XX microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
XX epilepsy; cancer; ss.
XX
XX Homo sapiens.
XX
XX MO200157275-A2.
XX
XX PD 09-AUG-2001.
XX
XX PF 30-JAN-2001; 2001WO-US00667.
XX
XX PR 04-FEB-2000; 2000US-0180312.
XX PR 26-MAY-2000; 2000US-0207456.
XX PR 30-JUN-2000; 2000US-0608408.
XX PR 03-AUG-2000; 2000US-0632366.
XX PR 21-SEP-2000; 2000US-0234687.
XX PR 27-SEP-2000; 2000US-0236359.
XX PR 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-483446/52.
XX
XX Single exon nucleic acid probes for analyzing gene expression in human
XX brains -
XX
```

XX Example 4; SEQ ID NO: 12466; 650bp + Sequence Listing; English.

CC The present invention provides a number of single exon nucleic acid
 CC probes which are derived from genomic sequences expressed in the human
 CC brain. They can be used to measure gene expression in brain cell samples,
 CC which may enable the diagnosis and improved treatment of nervous system
 CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
 CC epilepsy and cancers. The present sequence is one of the probes of the
 CC invention.

XX Sequence 581 BP; 115 A; 144 C; 201 G; 121 T; 0 other;

Query Match 1.6%; Score 18; DB 22; Length 581;

Best Local Similarity 100.0%; Pred. No. 68;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 43 ctgtgctgctgctgtct 60
 |||
 DB 168 CTGTGCTGCTGCTGCT 151

RESULT 11

AAK38184/C
 ID AAK38184 standard; DNA; 581 BP.

AC AAK38184;

XX 06-NOV-2001 (first entry)

DE Human bone marrow expressed single exon probe SEQ ID NO: 12741.

KM Human: bone marrow expressed exon; gene expression analysis; probe;
 KW microarray; cancer; leukemia; lymphoma; myeloma; ss.

XX Homo sapiens.

OS WO200157276-A2.

XX 09-AUG-2001.

PF 30-JAN-2001; 2001WO-US00668.

PR 04-FEB-2000; 2000US-0180312.

PR 26-MAY-2000; 2000US-0207456.

PR 30-JUN-2000; 2000US-0608408.

PR 03-AUG-2000; 2000US-0632366.

PR 21-SEP-2000; 2000US-0234467.

PR 27-SEP-2000; 2000US-0236359.

PR 04-OCT-2000; 2000GB-0024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488900/53.

DR Human genome-derived single exon nucleic acid probes useful for

XX analyzing gene expression in human bone marrow -

XX Example 4; SEQ ID NO: 12741; 658bp + Sequence Listing; English.

XX The present invention provides a number of single exon nucleic acid
 CC probes which are derived from genomic sequences expressed in the human
 CC bone marrow. They can be used to measure gene expression in bone marrow
 CC samples, which may enable the improved diagnosis and treatment of cancers
 CC such as lymphoma, leukemia and myeloma. The present sequence is one of
 CC the probes of the invention.

XX Sequence 581 BP; 115 A; 144 C; 201 G; 121 T; 0 other;

Query Match 1.6%; Score 18; DB 22; Length 581;
 Best Local Similarity 100.0%; Pred. No. 68;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 43 ctgtgctgctgctgtct 60
 |||
 DB 168 CTGTGCTGCTGCTGCT 151

RESULT 12

AA18978/C
 ID AA18978 standard; DNA; 581 BP.

AC AA18978;

DT 12-OCT-2001 (first entry)

DE Probe #8911 for gene expression analysis in human cervical cell sample.

KW Probe; human; microarray; gene expression; cervical epithelial cell;

KW cervical cancer; ss.

XX Homo sapiens.

OS WO200157278-A2.

XX 09-AUG-2001.

PF 30-JAN-2001; 2001WO-US00670.

PR 04-FEB-2000; 2000US-0180312.

PR 26-MAY-2000; 2000US-0207456.

PR 30-JUN-2000; 2000US-0608408.

PR 03-AUG-2000; 2000US-0632366.

PR 21-SEP-2000; 2000US-0234467.

PR 27-SEP-2000; 2000US-0236359.

PR 04-OCT-2000; 2000GB-0024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488901/53.

DR Human genome-derived single exon nucleic acid probes useful for

XX analyzing gene expression in human cervical epithelial cells -

XX Claim 25; SEQ ID NO 8911; 487bp; English.

CC The present invention relates to human single exon nucleic acid probes
 CC (SENPs). The present sequence is one such probe. The SENPs are derived
 CC from human HeLa cells. The SENPs can be used to produce a single exon
 CC microarray, which can be used for measuring human gene expression in a
 CC sample derived from human cervical epithelial cells. By measuring gene
 CC expression, the probes are therefore useful in grading and/or staging
 CC of diseases of the cervix, notably cervical cancer.

CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 581 BP; 115 A; 144 C; 201 G; 121 T; 0 other;

Query Match 1.6%; Score 18; DB 22; Length 581;

Best Local Similarity 100.0%; Pred. No. 68;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 43 ctgtgctgctgctgtct 60
 |||
 DB 168 CTGTGCTGCTGCTGCT 151

RESULT 13

```

AA14114/C
ID AA14114 standard; DNA; 581 BP.
XX
AC AA14114;
XX
DE 17-OCT-2001 (first entry)
XX
DE Probe #12800 used to measure gene expression in human placenta sample.
XX
KW Probe; microarray; human; placenta; antenatal diagnosis;
XX
KW genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN W0200157272-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000653.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI: 2001-488897/53.
XX
XX Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human placenta -
XX
XX
PS Claim 25; SEQ ID NO 12800; 654bp; English.
XX
CC The present invention relates to single exon nucleic acid probes (SENP).
CC The present sequence is one such probe. The probes are useful for
CC producing a microarray for predicting, measuring and displaying gene
CC expression in samples derived from human placenta. The probes are useful
CC for antenatal diagnosis of human genetic disorders.
XX
SQ Sequence 581 BP; 115 A; 144 C; 201 G; 121 T; 0 other;
SO

Query Match 1.6%; Score 18; DB 22; Length 581;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 43 ctgtgctgctgctgtct 60
| | | | | | | | | | | | | |
DB 168 CTGTCCTGCTGCTGCT 151

RESULT 14
AAFI2222
ID AAFI2222 standard; CDNA; 694 BP.
XX
AC AAFI2222;
XX
DE 13-MAR-2001 (first entry)
XX
DE Aspergillus oryzae EST SEQ ID NO:4745.
XX
KW Multiple gene expression; filamentous fungal cell; EST;
KW expressed sequence tag; Fusarium venenatum; Aspergillus niger;
KW Aspergillus oryzae; Trichoderma reesei; identification; recombination;
KW culture condition; environmental stress; spore morphogenesis;
KW metabolic pathway engineering; catabolic pathway engineering; ss.
XX

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OS Aspergillus oryzae.
XX
PN W0200056762-A2.
XX
PD 28-SEP-2000.
XX
PF 22-MAR-2000; 2000WO-US07781.
XX
PR 22-MAR-1999; 99US-0273623.
XX
PA (NOVO ) NOVO NORDISK BIOTECH INC.
XX
PA (NOVO ) NOVO NORDISK AS.
XX
PI Berka RM, Rey MM, Shuster JR, Kauppinen S, Clausen IG, Olsen PB;
XX
DR WPI: 2000-594572/56.
XX
DE
XX
PT Monitoring differential expression of genes in filamentous fungal cells
PT uses fluorescence-labeled nucleic acids isolated from the cells and a
PT substrate of expressed sequence tags -
XX
PS Claim 88; Page 2009-2010; 3161pp; English.
XX
CC The present invention describes a method for monitoring differential
CC expression of genes in a first filamentous fungal (FF) cell relative to
CC expression of the same genes in one or more second filamentous fungal
CC cells. The method uses fluorescence-labeled nucleic acids isolated from
CC the FF cells and a substrate of expressed sequence tags (EST). The ESTs
CC are used in the methods for monitoring differential expression of genes
CC in a first filamentous fungal (FF) cell relative to expression of the
CC same genes in one or more second filamentous fungal cells. Monitoring
CC the global expression of genes from FF cells allows the production
CC potential of the microorganisms to be improved. New genes may be
CC discovered, possible functions of unknown open reading frames can be
CC identified and gene copy number variation and stability can be
CC monitored. The expression of genes can be used to study how FF cells
CC adapt to changes in culture conditions, environmental stress, spore
CC morphogenesis, recombination, metabolic or catabolic pathway
CC engineering. Using ESTs provides several advantages over genomic or
CC random cDNA clones including elimination of redundancy as one spot on an
CC array equals one gene or open reading frame, and organization of the
CC microarrays based on function of the gene products to facilitate
CC analysis of the results. AAF07478 to AAF11247 represents ESTs from
CC Fusarium venenatum; AAF11248 to AAF11853 represents ESTs from Aspergillus
CC niger; AAF11854 to AAF14878 represents ESTs from Aspergillus oryzae; and
CC AAF14879 to AAF15337 represents ESTs from Trichoderma reesei, which are
CC all specifically claimed in the present invention.
XX
SQ Sequence 694 BP; 137 A; 225 C; 154 G; 177 T; 1 other;
SO

Query Match 1.6%; Score 18; DB 21; Length 694;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1056 cggcctggtgctctgtc 1073
| | | | | | | | | | | | | |
DB 490 cggcctggtgctctgtc 507

RESULT 15
AAS15814
ID AAS15814 standard; CDNA; 1396 BP.
XX
AC AAS15814;
XX
DE 16-JAN-2002 (first entry)
XX
DE Human cDNA encoding Six-Transmembrane Protein of Prostate 2, STMP2.
XX
KW Human; Six-Transmembrane Protein of Prostate 2; STMP2; prostate cancer;
KW benign prostatic hyperplasia; acute prostatitis; testicular cancer;
KW cryptorchidism; testicular disorder; proliferative disorder; lymphoma;
XX

```

KW leukaemia; melanoma; ovarian cancer; breast cancer; pancreatic cancer;
 XX liver cancer; lung cancer; cytostatic; ss.
 OS Homo sapiens.

Key	Location/Qualifiers
FT CDS	9..1388
FT	/*tag- a
FT	/product= "STMP2"
FT	/transl_except= (pos:372..374,aa:Xaa)
FT	/note= "Xaa= Ala or Thr"
FT	/transl_except= (pos:999..1001,aa:Xaa)
FT	/note= "Xaa= Pro or Leu"

WO200172962-A2.

04-OCT-2001.

23-MAR-2001; 2001WO-US09410.

24-MAR-2000; 2000US-191929P.

(SAAT/) SAATCLOGLU F.

Saatcloglu F;

WPI; 2001-662926/76.

P-PSDB; AAU10190.

New polynucleotide for the diagnosis, prevention and treatment for prostate and testis disorders, particularly prostate cancer, comprises prostate-specific or testis-specific nucleic acids -

Claim 4; Fig 4L; 114pp; English..

CC The invention relates to substantially pure prostate-specific or
 CC testis-specific polypeptides and the nucleic acids encoding them.
 CC Also included are vectors and host cells expressing the proteins, a
 CC transgenic animal expressing the protein, antibodies against the
 CC proteins, probes for detecting the nucleic acids, antisense molecules
 CC for the nucleic acids and methods of isolating modulators of the
 CC proteins. Compounds that modulate the prostate specific or testis
 CC specific polypeptide are useful to diagnose, prevent or treat disorders
 CC of the testis or prostate particularly prostate cancer, benign
 CC prostatic hyperplasia, acute prostatitis, testicular cancer,
 CC cryptorchidism, undescended, retractile, ascending or vanished
 CC testis. Other proliferative disorders for which the modulators may be
 CC used include lymphoma, leukaemia, melanoma, ovarian cancer, breast
 CC cancer, pancreatic cancer, liver cancer and lung cancer. The
 CC present sequence encodes a prostate specific protein, Six-Transmembrane
 CC Protein of Prostate 2, STMP2.

Sequence 1396 BP; 370 A; 312 C; 301 G; 413 T; 0 other;

Query Match

Best Local Similarity 1.6%; Score 18; DB 22; Length 1396;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY	33 tatttgctgctgtgctg 50
DB	621 tatttgctgctgtgctg 638

Search completed: May 7, 2002, 18:15:25
 Job time: 5247 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 7, 2002, 15:55:54 ; Search time 72.68 Seconds
(without alignments)
3842.671 Million cell updates/sec

Title: US-09-579-383-1
Perfect score: 1137
Sequence: 1 atgaatttaccgtaaataa.....tcgttgaaagctgcactaa 1137

Scoring table:
OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 38353 seqs, 122816752 residues

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Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

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5: /cgn2_6/ptodata/2/ina/PCrUS.COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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C 1	18	1.6	3416	2 US-08-451-822A-15	Sequence 15, Appl
C 2	18	1.6	3416	4 US-08-323-430-15	Sequence 3, Appl
C 3	18	1.6	6614	4 US-09-150-460B-3	Sequence 15, Appl
C 4	17	1.5	969	2 US-08-932-978-1	Sequence 1, Appl
C 5	17	1.5	2976	3 US-08-714-918-65	Sequence 65, Appl
C 6	17	1.5	2976	4 US-09-265-315-65	Sequence 65, Appl
C 7	17	1.5	2976	4 US-09-265-315-65	Sequence 65, Appl
C 8	17	1.5	2976	4 US-09-266-417-65	Sequence 65, Appl
C 9	17	1.5	6638	2 US-08-070-301-2	Sequence 2, Appl
C 10	17	1.5	40352	3 US-08-846-111D-15	Sequence 17, Appl
C 11	17	1.5	48974	4 US-08-920-422-17	Sequence 17, Appl
C 12	16	1.4	723	2 US-09-651-656-2	Sequence 2, Appl
C 13	16	1.4	1001	2 US-08-982-956-2	Sequence 2, Appl
C 14	16	1.4	1001	3 US-09-228-317-2	Sequence 2, Appl
C 15	16	1.4	1256	1 US-08-176-427B-9	Sequence 9, Appl
C 16	16	1.4	1256	2 US-08-356-060A-5	Sequence 5, Appl
C 17	16	1.4	1256	4 US-08-460-900C-5	Sequence 5, Appl
C 18	16	1.4	1256	4 US-08-674-509B-5	Sequence 5, Appl
C 19	16	1.4	1256	4 US-08-954-698-5	Sequence 5, Appl
C 20	16	1.4	1317	3 US-08-886-886-10	Sequence 10, Appl
C 21	16	1.4	1405	1 US-08-390-162-3	Sequence 3, Appl
C 22	16	1.4	1405	1 US-08-685-945B-3	Sequence 3, Appl
C 23	16	1.4	1713	2 US-08-386-727-5	Sequence 5, Appl
C 24	16	1.4	1713	2 US-08-600-452A-5	Sequence 5, Appl
C 25	16	1.4	2107	1 US-08-390-162-1	Sequence 1, Appl
C 26	16	1.4	2107	1 US-08-685-945B-1	Sequence 1, Appl
C 27	16	1.4	2158	1 US-07-688-352C-3	Sequence 3, Appl

28	16	1.4	2158	2 US-08-474-379C-3	Sequence 3, Appl
29	16	1.4	2158	3 US-09-146-249A-3	Sequence 3, Appl
30	16	1.4	2158	3 US-08-206-168B-3	Sequence 3, Appl
31	16	1.4	2158	5 PCT-US91-02714-3	Sequence 3, Appl
32	16	1.4	2223	1 US-08-257-073-4	Sequence 4, Appl
33	16	1.4	2262	1 US-07-689-008-3	Sequence 3, Appl
34	16	1.4	2274	3 US-08-492-459-13	Sequence 13, Appl
35	16	1.4	2274	3 US-08-423-752-13	Sequence 13, Appl
36	16	1.4	2274	4 US-08-716-873-27	Sequence 27, Appl
37	16	1.4	2274	4 US-09-368-431-27	Sequence 27, Appl
38	16	1.4	2274	4 US-08-233-146-8	Sequence 13, Appl
C 39	16	1.4	2456	1 US-08-463-470-8	Sequence 8, Appl
C 40	16	1.4	2456	1 US-08-804-439A-12	Sequence 12, Appl
C 41	16	1.4	2608	3 US-08-720-229-12	Sequence 12, Appl
C 42	16	1.4	2608	3 US-08-720-229-12	Sequence 12, Appl
C 43	16	1.4	2639	4 US-09-374-135-1	Sequence 1, Appl
C 44	16	1.4	2805	4 US-09-651-656-4	Sequence 4, Appl
C 45	16	1.4	2947	1 US-08-457-176-1	Sequence 1, Appl
C 46	16	1.4	2947	1 US-08-457-175-1	Sequence 1, Appl
C 47	16	1.4	3096	5 PCT-US96-05320A-897	Sequence 897, App
C 48	16	1.4	3209	1 US-07-803-633A-12	Sequence 12, Appl
C 49	16	1.4	3355	2 US-08-933-821-3	Sequence 3, Appl
C 50	16	1.4	3355	3 US-08-960-507-3	Sequence 3, Appl
C 51	16	1.4	3355	4 US-09-136-828-3	Sequence 3, Appl
C 52	16	1.4	4409	4 US-09-653-403-2	Sequence 8, Appl
C 53	16	1.4	4431	4 US-09-532-803-8	Sequence 8, Appl
C 54	16	1.4	5829	4 US-09-004-838-109	Sequence 109, App
C 55	16	1.4	6048	4 US-09-634-920-3	Sequence 3, Appl
C 56	16	1.4	6911	1 US-08-311-174-4	Sequence 4, Appl
C 57	16	1.4	9540	1 US-07-689-008-1	Sequence 1, Appl
C 58	16	1.4	2417	2 US-08-846-762-1	Sequence 1, Appl
C 59	16	1.4	68750	3 US-09-836-409-1	Sequence 1, Appl
C 60	16	1.4	68750	4 US-09-568-102-1	Sequence 1, Appl
C 61	16	1.4	68750	4 US-09-567-969-1	Sequence 1, Appl
C 62	16	1.4	68750	4 US-09-568-480-1	Sequence 1, Appl
C 63	16	1.4	68750	4 US-09-568-486-1	Sequence 1, Appl
C 64	16	1.4	68750	4 US-09-568-472-1	Sequence 1, Appl
C 65	16	1.4	71989	4 US-09-443-501A-2	Sequence 2, Appl
C 66	16	1.4	152331	3 US-09-128-155-16	Sequence 16, Appl
C 67	16	1.4	176373	3 US-09-128-155-17	Sequence 17, Appl
C 68	15	1.3	49	6 5240845-49	Patent No. 5240845
C 69	15	1.3	53	6 5240845-48	Patent No. 5240845
C 70	15	1.3	159	4 US-08-836-500A-7	Sequence 7, Appl
C 71	15	1.3	216	4 US-08-836-500A-5	Sequence 5, Appl
C 72	15	1.3	257	1 US-08-741-406-3	Sequence 3, Appl
C 73	15	1.3	257	3 US-09-024-472-3	Sequence 3, Appl
C 74	15	1.3	263	3 US-08-881-771A-6	Sequence 6, Appl
C 75	15	1.3	268	3 US-08-928-881-20	Sequence 20, Appl
C 76	15	1.3	321	4 US-09-199-637A-434	Sequence 434, App
C 77	15	1.3	401	4 US-08-328-111-761	Sequence 761, App
C 78	15	1.3	402	2 US-08-193-078B-20	Sequence 20, Appl
C 79	15	1.3	406	1 US-08-471-780C-99	Sequence 99, Appl
C 80	15	1.3	406	1 US-08-467-282B-99	Sequence 99, Appl
C 81	15	1.3	406	2 US-08-471-282A-99	Sequence 99, Appl
C 82	15	1.3	406	2 US-08-466-710C-99	Sequence 99, Appl
C 83	15	1.3	406	3 US-08-471-284B-99	Sequence 99, Appl
C 84	15	1.3	406	3 US-08-468-739C-99	Sequence 99, Appl
C 85	15	1.3	406	3 US-08-990-823-47	Sequence 47, Appl
C 86	15	1.3	489	4 US-09-199-637A-430	Sequence 430, App
C 87	15	1.3	510	4 US-08-432-994A-7	Sequence 7, Appl
C 88	15	1.3	537	4 US-08-836-500A-3	Sequence 3, Appl
C 89	15	1.3	607	1 US-08-061-314A-1	Sequence 1, Appl
C 90	15	1.3	622	4 US-08-858-207A-212	Sequence 212, App
C 91	15	1.3	651	2 US-08-929-418-1	Sequence 1, Appl
C 92	15	1.3	651	4 US-09-228-479-1	Sequence 1, Appl
C 93	15	1.3	676	4 US-08-998-416-1142	Sequence 1142, App
C 94	15	1.3	683	4 US-08-456-200B-1	Sequence 1, Appl
C 95	15	1.3	699	4 US-08-476-102A-6	Sequence 6, Appl
C 96	15	1.3	709	3 US-08-961-083-95	Sequence 95, Appl
C 97	15	1.3	717	4 US-08-998-416-586	Sequence 586, App
C 98	15	1.3	720	6 5229273-1	Patent No. 5229273
C 99	15	1.3	730	3 US-08-743-637B-11	Sequence 11, Appl
C 100	15	1.3	730	3 US-08-526-840B-11	Sequence 11, Appl

101	15	1.3	770	4	US-09-328-111-646	Sequence 646, App	c 174	15	1.3	2153	4	US-08-984-709A-19	Sequence 19, Appl
c 102	15	1.3	778	4	US-09-207-223-7	Sequence 7, Appl1	c 175	15	1.3	2212	3	US-08-960-507-18	Sequence 18, Appl
c 103	15	1.3	800	4	US-09-207-223-6	Sequence 6, Appl1	c 176	15	1.3	2381	2	US-08-736-770-4	Sequence 4, Appl1
c 104	15	1.3	868	3	US-08-961-083-19	Sequence 19, Appl1	c 177	15	1.3	2420	5	PCT-US93-000227-1	Sequence 1, Appl1
c 105	15	1.3	906	1	US-08-100-874-1	Sequence 1, Appl1	c 178	15	1.3	2540	2	US-08-511-485-3	Sequence 3, Appl1
c 106	15	1.3	937	4	US-09-532-656-13	Sequence 13, Appl1	c 179	15	1.3	2540	3	US-09-392-580-1	Sequence 1, Appl1
c 107	15	1.3	951	4	US-09-189-637A-432	Sequence 432, App	c 180	15	1.3	2625	2	US-08-468-036-2	Sequence 2, Appl1
c 108	15	1.3	1007	4	US-08-836-500A-1	Sequence 1, Appl1	c 181	15	1.3	2625	2	US-08-376-443-2	Sequence 2, Appl1
c 109	15	1.3	1008	3	US-08-721-979A-13	Sequence 13, Appl1	c 182	15	1.3	2691	3	US-09-212-971-9	Sequence 9, Appl1
c 110	15	1.3	1050	3	US-09-199-637A-428	Sequence 428, App	c 183	15	1.3	2691	3	US-08-800-929A-9	Sequence 9, Appl1
c 111	15	1.3	1072	5	US-08-096-181A-13	Sequence 13, Appl1	c 184	15	1.3	2691	3	US-09-617-053A-9	Sequence 9, Appl1
c 112	15	1.3	1072	5	PCT-US94-08326-13	Sequence 13, Appl1	c 185	15	1.3	2736	4	US-08-714-918-104	Sequence 104, App
c 113	15	1.3	1073	4	US-08-476-102A-1	Sequence 1, Appl1	c 186	15	1.3	2736	4	US-08-265-315-104	Sequence 104, App
c 114	15	1.3	1074	3	US-08-096-181A-11	Sequence 11, Appl1	c 187	15	1.3	2736	4	US-09-265-315-104	Sequence 104, App
c 115	15	1.3	1074	5	PCT-US94-08326-11	Sequence 11, Appl1	c 188	15	1.3	2736	4	US-09-265-315-104	Sequence 104, App
c 116	15	1.3	1077	4	US-08-945-515-1	Sequence 1, Appl1	c 189	15	1.3	2784	4	US-08-845-258-9	Sequence 9, Appl1
c 117	15	1.3	1096	3	US-08-881-771A-5	Sequence 5, Appl1	c 190	15	1.3	2784	4	US-08-990-571-9	Sequence 9, Appl1
c 118	15	1.3	1134	4	US-08-432-994A-9	Sequence 9, Appl1	c 191	15	1.3	2784	4	US-08-723-142A-9	Sequence 9, Appl1
c 119	15	1.3	1135	4	US-08-915-795-7	Sequence 7, Appl1	c 192	15	1.3	2802	1	US-08-215-805A-79	Sequence 79, Appl1
c 120	15	1.3	1137	3	US-08-096-181A-9	Sequence 9, Appl1	c 193	15	1.3	2980	4	US-08-456-200B-12	Sequence 12, Appl1
c 121	15	1.3	1137	5	PCT-US94-08326-9	Sequence 9, Appl1	c 194	15	1.3	3010	4	US-09-199-637A-168	Sequence 168, App
c 122	15	1.3	1207	3	US-08-872-979-4	Sequence 4, Appl1	c 195	15	1.3	3095	3	US-08-434-000A-7	Sequence 7, Appl1
c 123	15	1.3	1248	6	5240845-2	Patent No. 5240845	c 196	15	1.3	3095	4	US-09-312-157-7	Sequence 7, Appl1
c 124	15	1.3	1248	3	US-08-910-505-3	Sequence 3, Appl1	c 197	15	1.3	3172	1	US-08-314-309A-1	Sequence 1, Appl1
c 125	15	1.3	1251	3	US-08-910-505-1	Sequence 1, Appl1	c 198	15	1.3	3325	6	5240838-4	Patent No. 5240838
c 126	15	1.3	1262	6	5240845-3	Patent No. 5240845	c 199	15	1.3	3648	1	US-08-053-614-1	Sequence 1, Appl1
c 127	15	1.3	1335	4	US-08-915-795-6	Sequence 6, Appl1	c 200	15	1.3	3648	1	US-08-316-397B-1	Sequence 1, Appl1
c 128	15	1.3	1330	2	US-08-715-131-1	Sequence 1, Appl1	c 201	15	1.3	3648	2	US-09-034-306-1	Sequence 1, Appl1
c 129	15	1.3	1330	4	US-09-231-753-1	Sequence 1, Appl1	c 202	15	1.3	3648	5	US-09-259-437-1	Sequence 1, Appl1
c 130	15	1.3	1333	1	US-08-928-881-18	Sequence 18, Appl1	c 203	15	1.3	3648	5	PCT-US93-08782-1	Sequence 1, Appl1
c 131	15	1.3	1333	1	US-07-602-824A-1	Sequence 1, Appl1	c 204	15	1.3	3848	5	US-08-215-805A-1	Sequence 1, Appl1
c 132	15	1.3	1333	1	US-07-963-451-1	Sequence 1, Appl1	c 205	15	1.3	3999	2	US-08-971-244-1	Sequence 1, Appl1
c 133	15	1.3	1393	1	US-08-261-577-6	Sequence 6, Appl1	c 206	15	1.3	3999	4	US-09-183-846A-11	Sequence 11, Appl1
c 134	15	1.3	1420	2	US-08-909-965C-3	Sequence 3, Appl1	c 207	15	1.3	4220	4	US-09-183-846A-11	Sequence 11, Appl1
c 135	15	1.3	1464	1	US-07-735-062-11	Sequence 11, Appl1	c 208	15	1.3	4465	1	US-08-180-195-1	Sequence 1, Appl1
c 136	15	1.3	1464	1	US-08-469-202-11	Sequence 11, Appl1	c 209	15	1.3	4465	1	US-08-477-329-1	Sequence 1, Appl1
c 137	15	1.3	1464	2	US-08-484-434C-11	Sequence 11, Appl1	c 210	15	1.3	4465	2	US-08-475-458-1	Sequence 1, Appl1
c 138	15	1.3	1476	3	US-08-713-118-5	Sequence 5, Appl1	c 211	15	1.3	4465	4	US-08-960-400-1	Sequence 1, Appl1
c 139	15	1.3	1476	3	US-09-452-007-5	Sequence 5, Appl1	c 212	15	1.3	4465	4	US-09-583-459A-1	Sequence 1, Appl1
c 140	15	1.3	1477	5	US-08-096-181A-7	Sequence 7, Appl1	c 213	15	1.3	4465	4	US-09-583-459A-1	Sequence 1, Appl1
c 141	15	1.3	1477	5	PCT-US94-08326-7	Sequence 7, Appl1	c 214	15	1.3	4465	4	US-09-583-459A-1	Sequence 1, Appl1
c 142	15	1.3	1485	4	US-08-936-165A-218	Sequence 218, App	c 215	15	1.3	4781	2	US-09-331-581-1	Sequence 1, Appl1
c 143	15	1.3	1500	1	US-08-592-214A-15	Sequence 15, Appl1	c 216	15	1.3	4781	4	US-09-001-273-1	Sequence 1, Appl1
c 144	15	1.3	1500	3	US-08-659-188-15	Sequence 15, Appl1	c 217	15	1.3	4781	4	US-08-843-459A-1	Sequence 1, Appl1
c 145	15	1.3	1500	3	US-08-655-227-15	Sequence 15, Appl1	c 218	15	1.3	4821	1	US-08-053-614-3	Sequence 3, Appl1
c 146	15	1.3	1500	3	US-08-655-241-15	Sequence 15, Appl1	c 219	15	1.3	4821	1	US-08-316-397B-3	Sequence 3, Appl1
c 147	15	1.3	1500	3	US-09-149-976-15	Sequence 15, Appl1	c 220	15	1.3	4821	2	US-09-034-306-3	Sequence 3, Appl1
c 148	15	1.3	1500	4	US-09-398-326-15	Sequence 15, Appl1	c 221	15	1.3	4821	2	US-09-259-437-3	Sequence 3, Appl1
c 149	15	1.3	1525	1	US-08-609-572-1	Sequence 1, Appl1	c 222	15	1.3	4821	5	PCT-US93-08782-3	Sequence 3, Appl1
c 150	15	1.3	1525	4	US-08-841-751-1	Sequence 1, Appl1	c 223	15	1.3	4847	3	US-09-061-400-1	Sequence 1, Appl1
c 151	15	1.3	1525	4	US-08-846-340-1	Sequence 1, Appl1	c 224	15	1.3	4937	2	US-08-622-166A-3	Sequence 3, Appl1
c 152	15	1.3	1525	4	US-08-846-344-1	Sequence 1, Appl1	c 225	15	1.3	5232	3	US-09-212-971-3	Sequence 3, Appl1
c 153	15	1.3	1591	1	US-08-728-956-3	Sequence 3, Appl1	c 226	15	1.3	5232	3	US-08-800-929A-3	Sequence 3, Appl1
c 154	15	1.3	1608	2	US-08-622-166A-1	Sequence 1, Appl1	c 227	15	1.3	5427	4	US-09-617-053A-3	Sequence 3, Appl1
c 155	15	1.3	1678	2	US-08-976-259-11	Sequence 11, Appl1	c 228	15	1.3	5427	1	US-08-168-917-1	Sequence 1, Appl1
c 156	15	1.3	1751	2	US-08-955-138-3	Sequence 3, Appl1	c 229	15	1.3	5427	2	US-08-460-510-1	Sequence 1, Appl1
c 157	15	1.3	1791	1	US-08-565-386-10	Sequence 10, Appl1	c 230	15	1.3	5427	2	US-08-460-510-1	Sequence 1, Appl1
c 158	15	1.3	1830	1	US-08-343-733A-2	Sequence 2, Appl1	c 231	15	1.3	5427	2	US-08-460-510-1	Sequence 1, Appl1
c 159	15	1.3	1932	2	US-08-392-806A-1	Sequence 1, Appl1	c 232	15	1.3	5427	5	PCT-US92-00730-1	Sequence 1, Appl1
c 160	15	1.3	1932	4	US-09-257-490-1	Sequence 1, Appl1	c 233	15	1.3	5427	5	PCT-US92-00730-1	Sequence 1, Appl1
c 161	15	1.3	2026	2	US-08-149-097D-19	Sequence 19, Appl1	c 234	15	1.3	5648	5	PCT-US92-00862-1	Sequence 1, Appl1
c 162	15	1.3	2038	2	US-08-736-770-2	Sequence 2, Appl1	c 235	15	1.3	5648	2	US-09-371-008-1	Sequence 1, Appl1
c 163	15	1.3	2100	2	US-08-511-485-9	Sequence 9, Appl1	c 236	15	1.3	5687	2	US-08-380-403A-3	Sequence 3, Appl1
c 164	15	1.3	2126	2	US-08-789-354-1	Sequence 1, Appl1	c 237	15	1.3	5904	1	US-08-309-512-1	Sequence 1, Appl1
c 165	15	1.3	2126	3	US-09-110-937-1	Sequence 1, Appl1	c 238	15	1.3	5904	5	PCT-US92-08756A-1	Sequence 1, Appl1
c 166	15	1.3	2126	3	US-09-058-725B-1	Sequence 1, Appl1	c 239	15	1.3	5931	3	US-08-783-774-1	Sequence 1, Appl1
c 167	15	1.3	2126	3	US-09-232-857-1	Sequence 1, Appl1	c 240	15	1.3	5962	1	US-08-188-582-10	Sequence 10, Appl1
c 168	15	1.3	2144	2	US-08-149-097D-20	Sequence 20, Appl1	c 241	15	1.3	5962	1	US-08-646-715-10	Sequence 10, Appl1
c 169	15	1.3	2144	3	US-08-949-386-20	Sequence 20, Appl1	c 242	15	1.3	6681	4	US-08-976-259-65	Sequence 65, Appl1
c 170	15	1.3	2144	3	US-08-450-562-20	Sequence 20, Appl1	c 243	15	1.3	7125	1	US-07-745-206A-1	Sequence 1, Appl1
c 171	15	1.3	2144	4	US-08-984-709A-20	Sequence 20, Appl1	c 244	15	1.3	7125	2	US-08-311-563-1	Sequence 1, Appl1
c 172	15	1.3	2153	3	US-08-949-386-19	Sequence 19, Appl1	c 245	15	1.3	7286	3	US-09-331-581-3	Sequence 3, Appl1
c 173	15	1.3	2153	3	US-08-450-562-19	Sequence 19, Appl1	c 246	15	1.3	7635	1	US-08-455-543A-1	Sequence 1, Appl1

247	15	1.3	7635	1	US-08-455-543A-23	Sequence 23, Appl	c 320	14	1.2	89	3	US-08-722-719-15	Sequence 15, Appl
248	15	1.3	7635	2	US-08-193-078B-1	Sequence 1, Appl	c 321	14	1.2	163	1	US-08-248-474-25	Sequence 25, Appl
249	15	1.3	7635	2	US-08-193-078B-29	Sequence 29, Appl	c 322	14	1.2	163	3	US-08-756-849-25	Sequence 25, Appl
250	15	1.3	7635	2	US-08-223-305C-1	Sequence 1, Appl	c 323	14	1.2	176	4	US-08-991-789A-207	Sequence 207, App
251	15	1.3	7635	2	US-08-223-305C-23	Sequence 23, Appl	c 324	14	1.2	176	4	US-09-062-451-207	Sequence 207, App
252	15	1.3	7635	2	US-08-149-097D-1	Sequence 1, Appl	c 325	14	1.2	181	2	US-08-821-559A-6	Sequence 6, Appl
253	15	1.3	7635	3	US-08-949-386-1	Sequence 1, Appl	c 326	14	1.2	181	4	US-09-400-541-6	Sequence 40, Appl
254	15	1.3	7635	3	US-08-450-562-1	Sequence 1, Appl	c 327	14	1.2	249	1	US-07-872-644-40	Sequence 40, Appl
255	15	1.3	7635	3	US-08-984-709A-1	Sequence 1, Appl	c 328	14	1.2	249	1	US-08-297-494-40	Sequence 40, Appl
256	15	1.3	7938	3	US-09-331-581-14	Sequence 14, Appl	c 329	14	1.2	249	1	US-08-297-510-40	Sequence 40, Appl
257	15	1.3	8532	1	US-08-452-655B-1	Sequence 1, Appl	c 330	14	1.2	249	1	US-08-479-532-40	Sequence 40, Appl
258	15	1.3	8532	1	US-08-450-582-1	Sequence 1, Appl	c 331	14	1.2	249	1	US-08-453-526-40	Sequence 40, Appl
259	15	1.3	9606	3	US-07-741-940-1	Sequence 1, Appl	c 332	14	1.2	249	1	US-08-455-525-40	Sequence 40, Appl
260	15	1.3	9606	1	US-08-289-548A-1	Sequence 1, Appl	c 333	14	1.2	249	3	US-09-139-491-40	Sequence 40, Appl
261	15	1.3	9606	1	US-08-452-654-1	Sequence 1, Appl	c 334	14	1.2	249	5	PCT-US92-03222-140	Sequence 40, Appl
262	15	1.3	9606	2	US-08-370-235A-1	Sequence 1, Appl	c 335	14	1.2	278	4	US-09-060-756-3	Sequence 3, Appl
263	15	1.3	9717	4	US-09-251-645-1	Sequence 1, Appl	c 336	14	1.2	300	4	US-08-938-263-32	Sequence 22, Appl
264	15	1.3	10322	4	US-09-330-330-3	Sequence 3, Appl	c 337	14	1.2	309	4	US-09-221-298-4	Sequence 4, Appl
265	15	1.3	11459	4	US-09-454-721A-3	Sequence 3, Appl	c 338	14	1.2	313	4	US-08-976-259-110	Sequence 110, App
266	15	1.3	22671	4	US-08-976-259-14	Sequence 14, Appl	c 339	14	1.2	317	4	US-08-991-789A-181	Sequence 181, App
267	15	1.3	22846	2	US-08-469-461-3	Sequence 3, Appl	c 340	14	1.2	317	4	US-09-062-451-181	Sequence 1, Appl
268	15	1.3	22846	1	US-07-890-609-3	Sequence 3, Appl	c 341	14	1.2	320	4	US-09-481-161-1	Sequence 1, Appl
269	15	1.3	28958	1	US-08-258-261B-6	Sequence 6, Appl	c 342	14	1.2	321	4	US-09-087-465-21	Sequence 21, Appl
270	15	1.3	28958	1	US-08-456-837-6	Sequence 6, Appl	c 343	14	1.2	331	4	US-09-060-756-37	Sequence 347, App
271	15	1.3	28958	1	US-08-457-342-6	Sequence 6, Appl	c 344	14	1.2	334	2	US-08-875-972-17	Sequence 17, Appl
272	15	1.3	28958	1	US-08-457-666A-6	Sequence 6, Appl	c 345	14	1.2	386	4	US-09-060-756-364	Sequence 364, App
273	15	1.3	28958	1	US-08-458-076A-6	Sequence 6, Appl	c 346	14	1.2	389	4	US-09-481-161-3	Sequence 3, Appl
274	15	1.3	28958	1	US-08-764-233A-4	Sequence 4, Appl	c 347	14	1.2	404	1	US-08-223-616-21	Sequence 21, Appl
275	15	1.3	28958	1	US-08-457-335A-6	Sequence 6, Appl	c 348	14	1.2	404	5	PCT-US95-04228-21	Sequence 21, Appl
276	15	1.3	28958	1	US-08-729-214-6	Sequence 6, Appl	c 349	14	1.2	406	4	US-09-386-493-13	Sequence 13, Appl
277	15	1.3	28958	1	US-09-028-934-6	Sequence 6, Appl	c 350	14	1.2	423	1	US-08-470-179-135	Sequence 135, App
278	15	1.3	28958	3	US-09-302-812-38	Sequence 38, Appl	c 351	14	1.2	461	1	US-08-474-542A-278	Sequence 278, App
279	15	1.3	29793	4	US-09-511-477-38	Sequence 38, Appl	c 352	14	1.2	461	1	US-08-457-648-278	Sequence 278, App
280	15	1.3	35100	2	US-08-770-379-19	Sequence 19, Appl	c 353	14	1.2	490	5	PCT-US95-08295-23	Sequence 23, Appl
281	15	1.3	35100	4	US-08-757-669A-19	Sequence 19, Appl	c 354	14	1.2	537	2	US-08-627-508-3	Sequence 3, Appl
282	15	1.3	35100	4	US-09-230-371A-19	Sequence 19, Appl	c 355	14	1.2	545	4	US-09-227-357-149	Sequence 149, App
283	15	1.3	35524	3	US-08-923-137-1	Sequence 1, Appl	c 356	14	1.2	565	3	US-08-866-340-32	Sequence 32, Appl
284	15	1.3	37948	4	US-09-251-645-11	Sequence 11, Appl	c 357	14	1.2	565	4	US-09-103-875-38	Sequence 38, Appl
285	15	1.3	42235	4	US-09-199-637A-1	Sequence 1, Appl	c 358	14	1.2	578	2	US-08-619-542B-46	Sequence 46, Appl
286	15	1.3	43280	2	US-08-804-227C-1	Sequence 1, Appl	c 359	14	1.2	578	4	US-09-385-982-113	Sequence 113, App
287	15	1.3	49377	1	US-08-764-233A-1	Sequence 1, Appl	c 360	14	1.2	603	4	US-09-385-982-110	Sequence 110, App
288	15	1.3	59065	4	US-09-813-817-3	Sequence 3, Appl	c 361	14	1.2	617	4	US-09-328-111-577	Sequence 577, App
289	15	1.3	80161	4	US-09-036-987A-1	Sequence 1, Appl	c 362	14	1.2	617	4	US-09-385-982-222	Sequence 222, App
290	15	1.3	80161	4	US-09-370-700-1	Sequence 1, Appl	c 363	14	1.2	623	4	US-08-998-416-921	Sequence 921, App
291	15	1.3	87350	3	US-08-781-891-79	Sequence 79, Appl	c 364	14	1.2	627	3	US-09-181-183-9	Sequence 9, Appl
292	15	1.3	246240	2	US-08-724-394A-20	Sequence 20, Appl	c 365	14	1.2	627	4	US-09-277-700-9	Sequence 9, Appl
293	15	1.3	246240	2	US-08-724-394A-21	Sequence 21, Appl	c 366	14	1.2	629	2	US-08-670-186-1	Sequence 1, Appl
294	15	1.3	246240	2	US-08-724-394A-22	Sequence 22, Appl	c 367	14	1.2	630	4	US-08-646-695-13	Sequence 13, Appl
295	15	1.3	4403765	4	US-09-103-840A-2	Sequence 2, Appl	c 368	14	1.2	630	4	US-08-646-695-13	Sequence 13, Appl
296	15	1.3	4403765	4	US-09-103-840A-2	Sequence 2, Appl	c 369	14	1.2	630	5	PCT-US96-06053-13	Sequence 13, Appl
297	15	1.3	4411529	4	US-09-103-840A-1	Sequence 1, Appl	c 370	14	1.2	630	5	PCT-US96-06053-14	Sequence 14, Appl
298	15	1.3	4411529	4	US-09-339-993-32	Sequence 32, Appl	c 371	14	1.2	643	4	US-08-936-165A-247	Sequence 247, App
299	14	1.2	18	3	US-09-339-993-32	Sequence 32, Appl	c 372	14	1.2	643	4	US-08-861-774E-31	Sequence 31, Appl
300	14	1.2	24	1	US-08-559-303B-19	Sequence 19, Appl	c 373	14	1.2	645	4	US-08-998-416-997	Sequence 907, App
301	14	1.2	24	1	US-09-175-828-19	Sequence 19, Appl	c 374	14	1.2	668	1	US-08-516-545-1	Sequence 1, Appl
302	14	1.2	25	1	US-07-989-160-10	Sequence 10, Appl	c 375	14	1.2	677	4	US-09-328-111-281	Sequence 281, App
303	14	1.2	25	1	US-08-182-961B-33	Sequence 33, Appl	c 376	14	1.2	680	4	US-09-328-111-627	Sequence 627, App
304	14	1.2	25	4	US-09-007-678B-33	Sequence 33, Appl	c 377	14	1.2	689	1	US-08-106-507-9	Sequence 9, Appl
305	14	1.2	27	1	US-08-021-667A-11	Sequence 11, Appl	c 378	14	1.2	689	1	US-08-446-922-7	Sequence 7, Appl
306	14	1.2	27	1	US-08-410-544-11	Sequence 11, Appl	c 379	14	1.2	689	5	PCT-US93-10034-7	Sequence 7, Appl
307	14	1.2	27	1	US-08-728-785A-11	Sequence 11, Appl	c 380	14	1.2	703	4	US-08-856-207A-21	Sequence 21, Appl
308	14	1.2	30	1	US-08-089-910-1	Sequence 1, Appl	c 381	14	1.2	713	2	US-08-580-545B-7	Sequence 7, Appl
309	14	1.2	31	4	US-09-009-443-17	Sequence 17, Appl	c 382	14	1.2	713	4	US-09-262-653A-7	Sequence 7, Appl
310	14	1.2	35	1	US-08-087-772A-11	Sequence 11, Appl	c 383	14	1.2	714	4	US-08-971-090-2	Sequence 2, Appl
311	14	1.2	36	2	US-08-585-684B-1528	Sequence 1528, Ap	c 384	14	1.2	714	4	US-08-971-090-3	Sequence 3, Appl
312	14	1.2	36	2	US-08-585-684B-1585	Sequence 1585, Ap	c 385	14	1.2	720	4	US-08-998-416-1009	Sequence 1009, Ap
313	14	1.2	36	3	US-08-722-719-12	Sequence 12, Appl	c 386	14	1.2	766	4	US-08-998-416-1009	Sequence 395, App
314	14	1.2	36	3	US-08-722-719-31	Sequence 31, Appl	c 387	14	1.2	785	3	US-08-836-236-3	Sequence 3, Appl
315	14	1.2	36	4	US-09-038-073-1528	Sequence 1528, Ap	c 388	14	1.2	795	3	US-08-969-644-15	Sequence 15, Appl
316	14	1.2	36	4	US-09-038-073-1585	Sequence 1585, Ap	c 389	14	1.2	795	3	US-08-444-189-15	Sequence 15, Appl
317	14	1.2	37	1	US-08-403-762A-65	Sequence 65, App	c 390	14	1.2	795	3	US-08-468-544-15	Sequence 15, Appl
318	14	1.2	61	4	US-08-952-793-353	Sequence 353, App	c 391	14	1.2	807	3	US-08-871-483-10	Sequence 10, Appl
319	14	1.2	61	5	PCT-US96-09455A-353	Sequence 353, App	c 392	14	1.2	816	3	US-09-181-183-35	Sequence 35, Appl

C 393	14	1.2	816	4	US-09-277-700-35	Sequence 35, Appl	466	14	1.2	1250	2	US-08-455-736-39	Sequence 39, Appl
394	14	1.2	830	4	US-08-998-416-419	Sequence 43, App	467	14	1.2	1250	2	US-08-971-217-39	Sequence 39, Appl
395	14	1.2	846	2	US-08-619-542B-43	Sequence 419, Appl	468	14	1.2	1250	4	US-09-350-600-39	Sequence 39, Appl
396	14	1.2	913	1	US-08-109-391A-1	Sequence 1, Appl	469	14	1.2	1251	4	US-09-242-095-1	Sequence 1, Appl
397	14	1.2	913	1	US-08-459-019A-1	Sequence 1, Appl	C 470	14	1.2	1272	1	US-08-343-682-2	Sequence 2, Appl
398	14	1.2	913	2	US-08-460-428A-1	Sequence 1, Appl	C 471	14	1.2	1299	2	US-08-904-278-5	Sequence 5, Appl
399	14	1.2	913	3	US-08-458-860A-1	Sequence 1, Appl	C 472	14	1.2	1299	4	US-09-222-594-5	Sequence 5, Appl
C 400	14	1.2	926	1	US-08-106-507-1	Sequence 1, Appl	C 473	14	1.2	1301	2	US-08-467-948A-7	Sequence 7, Appl
401	14	1.2	929	3	US-08-860-368B-4	Sequence 4, Appl	474	14	1.2	1301	3	US-08-467-947A-7	Sequence 7, Appl
C 402	14	1.2	930	4	US-09-227-357-61	Sequence 61, Appl	475	14	1.2	1303	3	US-08-700-186-1	Sequence 1, Appl
403	14	1.2	930	4	US-09-227-357-146	Sequence 146, App	476	14	1.2	1303	2	US-08-914-981-1	Sequence 1, Appl
C 404	14	1.2	957	1	US-07-745-206A-16	Sequence 16, Appl	477	14	1.2	1303	3	US-09-116-115-1	Sequence 1, Appl
C 405	14	1.2	957	2	US-08-311-363-16	Sequence 16, Appl	478	14	1.2	1303	4	US-09-511-762-1	Sequence 1, Appl
406	14	1.2	998	4	US-09-122-400B-5	Sequence 5, Appl	479	14	1.2	1308	4	US-09-150-213-1	Sequence 1, Appl
C 407	14	1.2	998	4	US-09-132-400B-5	Sequence 5, Appl	480	14	1.2	1314	3	US-09-025-059-2	Sequence 2, Appl
408	14	1.2	1002	2	US-09-328-111-45	Sequence 445, App	481	14	1.2	1317	3	US-08-886-886-1	Sequence 1, Appl
C 409	14	1.2	1020	2	US-08-475-844-10	Sequence 10, Appl	482	14	1.2	1343	4	US-09-499-505-5	Sequence 5, Appl
C 410	14	1.2	1020	5	PCT-US95-08429-10	Sequence 10, Appl	483	14	1.2	1343	4	US-09-626-410-5	Sequence 5, Appl
411	14	1.2	1024	6	PCT-US95-16	Sequence 10, Appl	484	14	1.2	1343	4	US-09-116-188-5	Sequence 5, Appl
412	14	1.2	1027	4	US-09-276-531-24	Sequence 24, Appl	485	14	1.2	1343	4	US-09-626-410-5	Sequence 5, Appl
413	14	1.2	1032	4	US-09-146-319-1	Sequence 1, Appl	486	14	1.2	1345	2	US-08-702-153-3	Sequence 5, Appl
414	14	1.2	1032	4	US-09-175-973-1	Sequence 1, Appl	487	14	1.2	1345	2	US-08-626-343-5	Sequence 5, Appl
415	14	1.2	1038	4	US-09-004-838-128	Sequence 128, App	488	14	1.2	1356	4	US-09-371-913A-8	Sequence 3, Appl
416	14	1.2	1045	2	US-09-014-969-6	Sequence 1, Appl	489	14	1.2	1379	4	US-09-499-505-6	Sequence 6, Appl
417	14	1.2	1066	1	US-08-154-916-1	Sequence 1, Appl	490	14	1.2	1379	4	US-09-626-410-6	Sequence 6, Appl
418	14	1.2	1074	1	US-08-045-269C-3	Sequence 3, Appl	491	14	1.2	1379	4	US-09-116-188-6	Sequence 6, Appl
419	14	1.2	1074	3	US-08-371-680-3	Sequence 3, Appl	492	14	1.2	1379	4	US-09-626-047-6	Sequence 6, Appl
420	14	1.2	1074	5	PCT-US94-01198-3	Sequence 3, Appl	493	14	1.2	1379	4	US-09-626-343-6	Sequence 6, Appl
421	14	1.2	1075	3	US-09-116-115-16	Sequence 16, Appl	494	14	1.2	1380	4	US-09-499-505-4	Sequence 4, Appl
422	14	1.2	1075	4	US-09-341-762-16	Sequence 16, Appl	495	14	1.2	1380	4	US-09-626-410-4	Sequence 4, Appl
423	14	1.2	1094	4	US-09-149-918-3	Sequence 3, Appl	496	14	1.2	1380	4	US-09-116-188-4	Sequence 4, Appl
424	14	1.2	1095	2	US-09-139-424-1	Sequence 1, Appl	497	14	1.2	1380	4	US-09-626-047-4	Sequence 4, Appl
425	14	1.2	1096	1	US-08-525-507-4	Sequence 1, Appl	498	14	1.2	1380	4	US-09-626-343-4	Sequence 4, Appl
426	14	1.2	1121	1	US-08-207-412B-1	Sequence 1, Appl	499	14	1.2	1382	4	US-09-499-505-2	Sequence 2, Appl
427	14	1.2	1131	5	PCT-US95-02950-1	Sequence 1, Appl	500	14	1.2	1382	4	US-09-626-410-2	Sequence 2, Appl
428	14	1.2	1133	4	US-08-858-207A-3	Sequence 3, Appl	501	14	1.2	1382	4	US-09-116-188-2	Sequence 2, Appl
C 429	14	1.2	1140	2	US-08-904-278-7	Sequence 7, Appl	502	14	1.2	1382	4	US-09-626-047-2	Sequence 2, Appl
C 430	14	1.2	1140	3	US-09-222-594-7	Sequence 7, Appl	503	14	1.2	1384	3	US-09-626-343-2	Sequence 3, Appl
431	14	1.2	1158	3	US-08-860-368B-1	Sequence 1, Appl	C 504	14	1.2	1384	3	US-09-058-489-30	Sequence 30, Appl
432	14	1.2	1153	3	US-08-746-397-1	Sequence 1, Appl	505	14	1.2	1391	2	US-08-743-637B-7	Sequence 7, Appl
433	14	1.2	1157	1	US-07-960-985-1	Sequence 1, Appl	506	14	1.2	1391	3	US-08-526-840B-7	Sequence 7, Appl
434	14	1.2	1157	2	US-08-496-671-1	Sequence 1, Appl	507	14	1.2	1396	4	US-09-499-505-13	Sequence 13, Appl
435	14	1.2	1173	3	US-08-740-644-1	Sequence 1, Appl	508	14	1.2	1398	4	US-09-626-410-13	Sequence 13, Appl
C 436	14	1.2	1181	1	US-08-181-271A-27	Sequence 27, Appl	509	14	1.2	1398	4	US-09-116-188-13	Sequence 13, Appl
C 437	14	1.2	1181	1	US-08-449-315-27	Sequence 27, Appl	510	14	1.2	1398	4	US-09-626-047-13	Sequence 13, Appl
C 438	14	1.2	1181	1	US-08-444-803-27	Sequence 27, Appl	511	14	1.2	1398	4	US-09-626-343-13	Sequence 13, Appl
C 439	14	1.2	1181	1	US-08-449-043-27	Sequence 27, Appl	512	14	1.2	1400	4	US-09-144-918-1	Sequence 1, Appl
C 440	14	1.2	1181	1	US-08-456-265A-27	Sequence 27, Appl	513	14	1.2	1410	2	US-08-975-316-86	Sequence 86, Appl
C 441	14	1.2	1181	1	US-08-455-416-27	Sequence 27, Appl	C 514	14	1.2	1418	2	US-08-922-171-1	Sequence 1, Appl
C 442	14	1.2	1181	1	US-08-455-244-27	Sequence 27, Appl	515	14	1.2	1422	1	US-08-439-725A-1	Sequence 1, Appl
C 443	14	1.2	1181	1	US-08-454-876-27	Sequence 27, Appl	516	14	1.2	1422	2	US-08-867-471-1	Sequence 1, Appl
C 444	14	1.2	1181	2	US-08-457-364-27	Sequence 27, Appl	517	14	1.2	1422	3	US-08-705-245-18	Sequence 18, Appl
C 445	14	1.2	1181	2	US-08-456-262-27	Sequence 27, Appl	518	14	1.2	1422	5	PCT-US96-0666-1	Sequence 1, Appl
C 446	14	1.2	1181	2	US-08-456-340-27	Sequence 27, Appl	C 519	14	1.2	1428	2	US-08-904-278-3	Sequence 3, Appl
C 447	14	1.2	1181	2	US-08-455-736-27	Sequence 27, Appl	520	14	1.2	1428	4	US-09-222-594-3	Sequence 3, Appl
C 448	14	1.2	1181	2	US-08-971-217-27	Sequence 27, Appl	521	14	1.2	1430	4	US-09-499-505-3	Sequence 3, Appl
C 449	14	1.2	1181	2	US-09-350-600-27	Sequence 27, Appl	C 522	14	1.2	1430	4	US-09-357-251-17	Sequence 17, Appl
450	14	1.2	1197	3	US-08-935-263-11	Sequence 11, Appl	523	14	1.2	1430	4	US-09-626-410-3	Sequence 3, Appl
C 451	14	1.2	1206	4	US-08-861-774E-13	Sequence 13, Appl	524	14	1.2	1430	4	US-09-116-188-3	Sequence 3, Appl
C 452	14	1.2	1221	3	US-08-965-600-2	Sequence 2, Appl	525	14	1.2	1430	4	US-09-626-047-3	Sequence 3, Appl
C 453	14	1.2	1224	4	US-09-574-942-1	Sequence 1, Appl	526	14	1.2	1430	4	US-09-626-343-3	Sequence 3, Appl
C 454	14	1.2	1237	4	US-09-007-678B-48	Sequence 48, Appl	C 527	14	1.2	1430	2	US-08-692-787-6	Sequence 6, Appl
455	14	1.2	1250	1	US-08-181-271A-39	Sequence 39, Appl	C 528	14	1.2	1478	1	US-08-700-359-3	Sequence 3, Appl
456	14	1.2	1250	1	US-08-449-315-39	Sequence 39, Appl	529	14	1.2	1485	4	US-09-499-505-1	Sequence 1, Appl
457	14	1.2	1250	1	US-08-444-803-39	Sequence 39, Appl	530	14	1.2	1485	4	US-09-626-410-1	Sequence 1, Appl
458	14	1.2	1250	1	US-08-449-043-39	Sequence 39, Appl	531	14	1.2	1485	4	US-09-116-188-1	Sequence 1, Appl
459	14	1.2	1250	1	US-08-456-265A-39	Sequence 39, Appl	532	14	1.2	1485	4	US-09-626-047-1	Sequence 1, Appl
460	14	1.2	1250	1	US-08-455-416-39	Sequence 39, Appl	533	14	1.2	1485	4	US-09-626-343-1	Sequence 1, Appl
461	14	1.2	1250	1	US-08-455-244-39	Sequence 39, Appl	534	14	1.2	1516	3	US-08-307-896-2	Sequence 2, Appl
462	14	1.2	1250	1	US-08-454-876-39	Sequence 39, Appl	535	14	1.2	1516	3	US-09-344-914-1	Sequence 1, Appl
463	14	1.2	1250	2	US-08-457-364-39	Sequence 39, Appl	536	14	1.2	1528	4	US-08-936-165A-200	Sequence 200, App
464	14	1.2	1250	2	US-08-456-262-39	Sequence 39, Appl	537	14	1.2	1545	1	US-07-621-670-1	Sequence 1, Appl
465	14	1.2	1250	2	US-08-456-240-39	Sequence 39, Appl	538	14	1.2	1546	3	US-08-961-083-21	Sequence 21, Appl

539	14	1.2	1552	2	US-08-752-760A-3	Sequence 3, Appli	612	14	1.2	2294	2	US-08-676-279-49	Sequence 49, Appli
540	14	1.2	1553	3	US-08-492-459-21	Sequence 21, Appli	C 613	14	1.2	2303	2	US-08-480-229C-9	Sequence 9, Appli
541	14	1.2	1553	3	US-08-423-752-21	Sequence 21, Appli	C 614	14	1.2	2303	2	US-08-659-235C-9	Sequence 9, Appli
542	14	1.2	1553	4	US-08-716-873-35	Sequence 35, Appli	C 615	14	1.2	2308	2	US-08-480-229C-28	Sequence 28, Appli
543	14	1.2	1553	4	US-09-368-431-35	Sequence 35, Appli	C 616	14	1.2	2308	2	US-08-659-235C-28	Sequence 28, Appli
544	14	1.2	1553	4	US-09-414-006-21	Sequence 21, Appli	C 617	14	1.2	2338	2	US-08-425-069-1	Sequence 1, Appli
545	14	1.2	1554	3	US-08-045-269C-1	Sequence 1, Appli	C 618	14	1.2	2338	2	US-08-317-844B-1	Sequence 1, Appli
546	14	1.2	1554	3	US-08-371-680-1	Sequence 1, Appli	C 619	14	1.2	2339	5	PCT-US92-09325-3	Sequence 3, Appli
547	14	1.2	1554	5	PCT-US94-01198-1	Sequence 1, Appli	C 620	14	1.2	2340	5	PCT-US92-09325-1	Sequence 1, Appli
548	14	1.2	1558	5	PCT-US95-11808-2	Sequence 2, Appli	C 621	14	1.2	2349	2	US-08-184-009-145	Sequence 145, App
549	14	1.2	1571	1	US-08-726-525-1	Sequence 1, Appli	622	14	1.2	2349	2	US-08-458-356-145	Sequence 145, App
550	14	1.2	1571	1	US-08-487-942-1	Sequence 1, Appli	623	14	1.2	2349	4	US-08-460-726-145	Sequence 145, App
551	14	1.2	1571	2	US-08-726-036A-1	Sequence 1, Appli	C 624	14	1.2	2383	4	US-08-232-358-18	Sequence 18, App
552	14	1.2	1571	4	US-09-083-516-1	Sequence 1, Appli	C 625	14	1.2	2383	4	US-08-786-164-18	Sequence 18, Appli
553	14	1.2	1573	3	US-09-249-336-1	Sequence 1, Appli	C 626	14	1.2	2413	2	US-09-518-046-1	Sequence 1, Appli
554	14	1.2	1573	4	US-09-249-338-1	Sequence 1, Appli	627	14	1.2	2416	1	US-09-261-416-1	Sequence 1, Appli
555	14	1.2	1584	4	US-09-318-448-31	Sequence 31, Appli	628	14	1.2	2434	2	US-08-184-009-144	Sequence 144, App
C 556	14	1.2	1593	2	US-08-524-828-2	Sequence 2, Appli	C 629	14	1.2	2434	2	US-08-458-356-144	Sequence 144, App
C 557	14	1.2	1593	2	US-08-975-114A-2	Sequence 2, Appli	C 630	14	1.2	2434	4	US-08-460-736-144	Sequence 144, App
C 558	14	1.2	1593	2	US-08-849-281A-2	Sequence 2, Appli	C 631	14	1.2	2457	2	US-08-486-013-68	Sequence 68, App
C 559	14	1.2	1601	3	US-08-735-491-1	Sequence 1, Appli	C 632	14	1.2	2457	2	US-08-482-279-68	Sequence 68, Appli
C 560	14	1.2	1608	2	US-08-855-518-2	Sequence 2, Appli	C 633	14	1.2	2457	2	US-08-342-268-68	Sequence 68, Appli
C 561	14	1.2	1617	2	US-08-540-118-2	Sequence 2, Appli	C 634	14	1.2	2457	3	US-09-015-968-68	Sequence 68, Appli
C 562	14	1.2	1649	1	US-07-688-352C-35	Sequence 35, Appli	C 635	14	1.2	2457	4	US-09-397-386-68	Sequence 68, Appli
563	14	1.2	1649	2	US-08-474-379C-35	Sequence 35, Appli	C 636	14	1.2	2485	4	US-08-637-823B-1	Sequence 1, Appli
564	14	1.2	1649	3	US-09-146-249A-35	Sequence 35, Appli	C 637	14	1.2	2493	3	US-08-945-056-3	Sequence 3, Appli
565	14	1.2	1649	3	US-08-206-188B-35	Sequence 35, Appli	C 638	14	1.2	2544	3	US-09-518-046-3	Sequence 3, Appli
566	14	1.2	1649	5	PCT-US91-02714-34	Sequence 34, Appli	C 639	14	1.2	2551	2	US-08-486-013-70	Sequence 70, Appli
567	14	1.2	1664	3	US-09-339-993-1	Sequence 1, Appli	C 640	14	1.2	2551	2	US-08-482-279-70	Sequence 70, Appli
C 568	14	1.2	1697	1	US-08-343-027A-1	Sequence 1, Appli	C 641	14	1.2	2551	2	US-08-342-268-70	Sequence 70, Appli
569	14	1.2	1703	4	US-09-370-253-9	Sequence 9, Appli	C 642	14	1.2	2551	4	US-09-015-968-70	Sequence 70, Appli
570	14	1.2	1725	2	US-08-907-166-11	Sequence 11, Appli	C 643	14	1.2	2551	3	US-09-397-386-70	Sequence 70, Appli
571	14	1.2	1725	2	US-08-932-376A-1	Sequence 1, Appli	C 644	14	1.2	2577	4	US-08-628-434-1	Sequence 1, Appli
572	14	1.2	1746	3	US-08-951-130-5	Sequence 5, Appli	645	14	1.2	2600	4	US-08-628-434-1	Sequence 1, Appli
C 573	14	1.2	1764	2	US-08-918-723-2	Sequence 2, Appli	646	14	1.2	2607	1	US-08-369-796-5	Sequence 5, Appli
C 574	14	1.2	1764	2	US-09-237-507-2	Sequence 2, Appli	647	14	1.2	2607	1	US-08-852-091-5	Sequence 5, Appli
575	14	1.2	1767	1	US-08-930-894-1	Sequence 1, Appli	648	14	1.2	2607	2	US-08-820-754-5	Sequence 5, Appli
576	14	1.2	1788	1	US-08-035-928-1	Sequence 1, Appli	649	14	1.2	2607	3	US-08-956-662-5	Sequence 5, Appli
C 577	14	1.2	1789	1	US-08-455-543A-29	Sequence 1, Appli	650	14	1.2	2607	3	US-08-956-869-5	Sequence 5, Appli
C 578	14	1.2	1789	2	US-08-223-305C-29	Sequence 29, Appli	651	14	1.2	2607	3	US-08-948-547-5	Sequence 5, Appli
579	14	1.2	1848	2	US-08-622-740-7	Sequence 7, Appli	652	14	1.2	2607	4	US-08-956-653A-5	Sequence 5, Appli
580	14	1.2	1848	3	US-08-440-689-7	Sequence 7, Appli	653	14	1.2	2607	5	PCT-US95-17025-5	Sequence 5, Appli
581	14	1.2	1848	4	US-09-122-399-7	Sequence 7, Appli	654	14	1.2	2657	1	US-07-718-535-2	Sequence 2, Appli
582	14	1.2	1904	2	US-08-933-750C-95	Sequence 95, Appli	655	14	1.2	2657	1	US-08-161-999-2	Sequence 2, Appli
583	14	1.2	1904	3	US-09-234-613-95	Sequence 95, Appli	C 656	14	1.2	2671	5	US-08-408-519-1	Sequence 1, Appli
C 584	14	1.2	1921	3	US-08-482-677-3	Sequence 3, Appli	C 657	14	1.2	2671	5	PCT-US95-03552-1	Sequence 1, Appli
C 585	14	1.2	1926	1	US-08-152-019A-43	Sequence 43, Appli	658	14	1.2	2682	2	US-08-867-941-7	Sequence 7, Appli
586	14	1.2	1950	2	US-08-472-659-30	Sequence 30, Appli	C 659	14	1.2	2682	2	US-08-867-941-7	Sequence 7, Appli
587	14	1.2	1950	2	US-08-474-661-30	Sequence 30, Appli	C 660	14	1.2	2682	4	US-09-074-658-7	Sequence 7, Appli
588	14	1.2	1950	2	US-08-611-977-30	Sequence 30, Appli	C 661	14	1.2	2682	4	US-09-074-658-7	Sequence 7, Appli
589	14	1.2	1964	1	US-08-132-168A-31	Sequence 31, Appli	662	14	1.2	2694	2	US-08-867-941-2	Sequence 2, Appli
590	14	1.2	1964	4	US-08-687-590-57	Sequence 57, Appli	C 663	14	1.2	2694	4	US-08-867-941-2	Sequence 2, Appli
591	14	1.2	2019	3	US-08-926-636-1	Sequence 1, Appli	C 664	14	1.2	2694	4	US-09-074-658-2	Sequence 2, Appli
592	14	1.2	2019	4	US-09-282-305-5	Sequence 5, Appli	C 665	14	1.2	2694	4	US-09-074-658-2	Sequence 2, Appli
593	14	1.2	2031	1	US-08-217-299-2	Sequence 2, Appli	C 666	14	1.2	2700	3	US-09-022-875-1	Sequence 1, Appli
C 594	14	1.2	2074	4	US-08-630-915A-19	Sequence 19, Appli	667	14	1.2	2746	2	US-09-016-000-12	Sequence 12, Appli
595	14	1.2	2097	2	US-08-602-725-35	Sequence 35, Appli	C 668	14	1.2	2756	1	US-08-187-793-3	Sequence 3, Appli
596	14	1.2	2167	4	US-09-489-869-10	Sequence 10, Appli	C 669	14	1.2	2784	1	US-08-104-073-3	Sequence 3, Appli
597	14	1.2	2220	1	US-08-389-459A-16	Sequence 16, Appli	C 670	14	1.2	2784	2	US-08-351-413-10	Sequence 10, Appli
598	14	1.2	2220	3	US-08-932-376A-3	Sequence 3, Appli	C 671	14	1.2	2784	2	US-09-025-583-10	Sequence 10, Appli
599	14	1.2	2220	3	US-08-967-867A-16	Sequence 16, Appli	C 672	14	1.2	2799	3	US-08-968-752B-5	Sequence 5, Appli
C 600	14	1.2	2238	4	US-08-939-366-5	Sequence 5, Appli	673	14	1.2	2839	3	US-08-468-856B-5	Sequence 5, Appli
C 601	14	1.2	2242	3	US-09-400-742-1	Sequence 1, Appli	674	14	1.2	3046	1	US-08-468-859A-5	Sequence 5, Appli
C 602	14	1.2	2242	4	US-08-618-651A-1	Sequence 1, Appli	675	14	1.2	3046	1	US-08-525-507-7	Sequence 7, Appli
C 603	14	1.2	2242	4	US-09-215-252-1	Sequence 1, Appli	676	14	1.2	3133	4	US-09-103-069-1	Sequence 1, Appli
C 604	14	1.2	2247	2	US-08-524-828-1	Sequence 1, Appli	C 677	14	1.2	3164	1	US-08-188-228-19	Sequence 19, Appli
C 605	14	1.2	2247	2	US-08-975-114A-1	Sequence 1, Appli	C 678	14	1.2	3164	1	US-08-332-643-43	Sequence 43, Appli
C 606	14	1.2	2264	1	US-08-232-538-16	Sequence 16, Appli	C 679	14	1.2	3164	1	US-08-332-638-49	Sequence 49, Appli
C 607	14	1.2	2264	4	US-08-786-164-16	Sequence 16, Appli	680	14	1.2	3166	2	US-07-688-352C-23	Sequence 23, Appli
C 608	14	1.2	2276	4	US-08-637-823B-24	Sequence 24, Appli	681	14	1.2	3166	2	US-08-474-379C-23	Sequence 23, Appli
609	14	1.2	2276	4	US-07-861-458C-38	Sequence 38, Appli	682	14	1.2	3166	3	US-09-146-249A-23	Sequence 23, Appli
610	14	1.2	2280	3	US-09-272-114A-2	Sequence 2, Appli	683	14	1.2	3186	3	US-08-206-188B-23	Sequence 23, Appli
C 611	14	1.2	2292	4	US-09-142-956B-1	Sequence 1, Appli	684	14	1.2	3186	5	PCT-US91-02714-22	Sequence 22, Appli

685	14	1.2	3205	4	US-09-651-656-102	Sequence 102, App	758	14	1.2	4068	3	US-09-146-249A-58	Sequence 58, Appl
686	14	1.2	3234	1	US-08-286-325A-7	Sequence 7, Appl1	759	14	1.2	4068	3	US-08-206-188B-58	Sequence 58, Appl
C 687	14	1.2	3250	3	US-08-617-860B-1	Sequence 1, Appl1	C 760	14	1.2	4071	4	US-09-098-707B-1	Sequence 1, Appl1
C 688	14	1.2	3293	2	US-08-442-809A-75	Sequence 75, Appl	C 761	14	1.2	4071	4	US-09-483-539-1	Sequence 1, Appl1
C 689	14	1.2	3295	4	US-09-336-447A-8	Sequence 8, Appl1	C 762	14	1.2	4106	4	US-08-434-823-1	Sequence 1, Appl1
C 690	14	1.2	3318	1	US-08-187-793-3	Sequence 3, Appl1	C 763	14	1.2	4106	1	US-08-457-366-1	Sequence 1, Appl1
C 691	14	1.2	3350	3	US-08-617-860B-3	Sequence 2, Appl1	C 764	14	1.2	4131	1	US-07-872-444-38	Sequence 38, Appl
C 692	14	1.2	3358	3	US-09-248-571-2	Sequence 2, Appl1	C 765	14	1.2	4131	1	US-08-297-494-38	Sequence 38, Appl
C 693	14	1.2	3393	4	US-09-104-324B-1	Sequence 1, Appl1	C 766	14	1.2	4131	1	US-08-297-494-38	Sequence 38, Appl
C 694	14	1.2	3393	4	US-09-162-713-1	Sequence 1, Appl1	C 767	14	1.2	4131	1	US-08-485-588-4	Sequence 4, Appl1
C 695	14	1.2	3450	2	US-08-545-562A-6	Sequence 6, Appl1	C 768	14	1.2	4131	1	US-08-484-565-4	Sequence 4, Appl1
C 696	14	1.2	3466	3	US-09-027-166-10	Sequence 10, Appl	C 769	14	1.2	4131	1	US-08-479-532-38	Sequence 38, Appl
C 697	14	1.2	3494	4	US-08-976-259-84	Sequence 84, Appl	C 770	14	1.2	4131	1	US-08-455-526-38	Sequence 38, Appl
C 698	14	1.2	3546	2	US-09-097-767A-37	Sequence 37, Appl1	C 771	14	1.2	4131	1	US-08-455-525-38	Sequence 38, Appl
C 699	14	1.2	3544	2	US-08-485-139-3	Sequence 3, Appl1	C 772	14	1.2	4131	2	US-08-480-751-4	Sequence 4, Appl1
C 700	14	1.2	3544	3	US-08-750-357-3	Sequence 3, Appl1	C 773	14	1.2	4131	2	US-08-943-986-4	Sequence 4, Appl1
C 701	14	1.2	3558	3	US-08-894-440-3	Sequence 3, Appl1	C 774	14	1.2	4131	2	US-08-353-784-4	Sequence 3, Appl1
C 702	14	1.2	3658	4	US-09-458-093-3	Sequence 3, Appl1	C 775	14	1.2	4131	3	US-09-139-491-38	Sequence 38, Appl
C 703	14	1.2	3704	2	US-08-702-153-1	Sequence 1, Appl1	C 776	14	1.2	4131	3	US-08-484-719B-4	Sequence 4, Appl1
C 704	14	1.2	3751	2	US-08-609-230A-8	Sequence 8, Appl1	C 777	14	1.2	4131	4	US-08-484-159-4	Sequence 4, Appl1
C 705	14	1.2	3751	2	US-07-872-644-42	Sequence 42, Appl	C 778	14	1.2	4131	5	PCT-US92-03222-38	Sequence 38, Appl
C 706	14	1.2	3789	1	US-08-297-494-42	Sequence 42, Appl	C 779	14	1.2	4140	3	US-08-694-731-2	Sequence 2, Appl1
C 707	14	1.2	3789	1	US-08-297-510-42	Sequence 42, Appl	C 780	14	1.2	4235	1	US-08-021-601-3	Sequence 1, Appl1
C 708	14	1.2	3789	1	US-08-479-532-42	Sequence 42, Appl	C 781	14	1.2	4235	1	US-08-082-849B-3	Sequence 3, Appl1
C 709	14	1.2	3789	1	US-08-455-526-42	Sequence 42, Appl	C 782	14	1.2	4235	5	PCT-US94-01624-3	Sequence 3, Appl1
C 710	14	1.2	3789	1	US-08-455-525-42	Sequence 42, Appl	C 783	14	1.2	4236	1	US-08-810-116-7	Sequence 7, Appl1
C 711	14	1.2	3789	3	US-09-139-491-42	Sequence 42, Appl	C 784	14	1.2	4236	2	US-07-930-548A-7	Sequence 7, Appl1
C 712	14	1.2	3789	5	PCT-US92-03222-42	Sequence 42, Appl	C 785	14	1.2	4284	4	US-08-525-507-14	Sequence 14, Appl1
C 713	14	1.2	3796	2	US-08-762-308-11	Sequence 11, Appl	C 786	14	1.2	4286	4	US-09-413-304-7	Sequence 7, Appl1
C 714	14	1.2	3813	6	US-08-650-000-3	Sequence 3, Appl1	C 787	14	1.2	4291	3	US-08-417-210A-81	Sequence 81, Appl
C 715	14	1.2	3813	6	5395760-3	Patent No. 3395760	C 788	14	1.2	4337	3	US-09-187-049-1	Sequence 1, Appl1
C 716	14	1.2	3814	4	US-09-302-812-5	Sequence 5, Appl1	C 789	14	1.2	4337	1	US-08-559-303B-72	Sequence 72, Appl
C 717	14	1.2	3814	4	US-09-511-477-5	Sequence 5, Appl1	C 790	14	1.2	4437	4	US-09-175-828-72	Sequence 72, Appl
C 718	14	1.2	3820	3	US-08-990-140-3	Sequence 3, Appl1	C 791	14	1.2	4465	1	US-08-180-195-1	Sequence 1, Appl1
C 719	14	1.2	3820	1	US-09-546-238-3	Sequence 3, Appl1	C 792	14	1.2	4465	1	US-08-477-329-1	Sequence 1, Appl1
C 720	14	1.2	3827	1	US-08-170-294-6	Sequence 6, Appl1	C 793	14	1.2	4465	2	US-08-475-458-1	Sequence 1, Appl1
C 721	14	1.2	3827	2	US-08-664-855-6	Sequence 6, Appl1	C 794	14	1.2	4465	3	US-08-980-400-1	Sequence 1, Appl1
C 722	14	1.2	3827	2	US-08-718-751-1	Sequence 1, Appl1	C 795	14	1.2	4465	4	US-09-583-459A-1	Sequence 1, Appl1
C 723	14	1.2	3827	3	US-09-049-289-6	Sequence 6, Appl1	C 796	14	1.2	4465	4	US-09-583-410-1	Sequence 1, Appl1
C 724	14	1.2	3829	2	US-08-631-097-8	Sequence 8, Appl1	C 797	14	1.2	4465	4	US-09-583-449A-1	Sequence 1, Appl1
C 725	14	1.2	3829	4	US-08-810-712-6	Sequence 6, Appl1	C 798	14	1.2	4490	4	US-09-476-366A-1	Sequence 1, Appl1
C 726	14	1.2	3867	4	US-09-347-114A-81	Sequence 81, Appl	C 799	14	1.2	4592	1	US-08-472-934-9	Sequence 9, Appl1
C 727	14	1.2	3880	2	US-08-942-521B-1	Sequence 1, Appl1	C 800	14	1.2	4592	2	US-08-323-460A-9	Sequence 9, Appl1
C 728	14	1.2	3880	3	US-09-192-702-1	Sequence 1, Appl1	C 801	14	1.2	4592	2	US-08-461-146C-9	Sequence 9, Appl1
C 729	14	1.2	3890	5	PCT-US94-02612-1	Sequence 1, Appl1	C 802	14	1.2	4592	2	US-08-461-1455-1	Sequence 9, Appl1
C 730	14	1.2	3890	5	US-08-445-474-1	Sequence 1, Appl1	C 803	14	1.2	4629	3	US-08-484-891-7	Sequence 7, Appl1
C 731	14	1.2	3913	2	US-08-472-934-7	Sequence 7, Appl1	C 804	14	1.2	4656	4	US-09-425-665-1	Sequence 1, Appl1
C 732	14	1.2	3913	2	US-08-323-460A-7	Sequence 7, Appl1	C 805	14	1.2	4656	4	US-09-685-668-1	Sequence 1, Appl1
C 733	14	1.2	3913	2	US-08-461-146C-7	Sequence 7, Appl1	C 806	14	1.2	4670	3	US-08-717-294-41	Sequence 41, Appl
C 734	14	1.2	3913	3	US-08-461-145C-7	Sequence 7, Appl1	C 807	14	1.2	4758	3	US-09-191-647-1	Sequence 1, Appl1
C 735	14	1.2	3913	4	US-08-628-829-11	Sequence 11, Appl	C 808	14	1.2	4758	4	US-09-540-245A-1	Sequence 1, Appl1
C 736	14	1.2	3943	2	US-08-369-796-3	Sequence 3, Appl1	C 809	14	1.2	4758	4	US-09-540-153-1	Sequence 1, Appl1
C 737	14	1.2	3943	2	US-08-852-091-3	Sequence 3, Appl1	C 810	14	1.2	4771	3	US-08-840-062-3	Sequence 3, Appl1
C 738	14	1.2	3943	2	US-08-820-754-3	Sequence 3, Appl1	C 811	14	1.2	4800	5	PCT-US94-07779-1	Sequence 1, Appl1
C 739	14	1.2	3943	2	US-08-856-652-3	Sequence 3, Appl1	C 812	14	1.2	4951	2	US-08-867-030B-5	Sequence 5, Appl1
C 740	14	1.2	3943	3	US-08-556-869-3	Sequence 3, Appl1	C 813	14	1.2	4951	2	PCT-US95-06119-5	Sequence 5, Appl1
C 741	14	1.2	3943	3	US-08-948-547-3	Sequence 3, Appl1	C 814	14	1.2	4954	1	US-08-920-812-18	Sequence 18, Appl
C 742	14	1.2	3943	4	US-09-364-970-10	Sequence 10, Appl	C 815	14	1.2	4954	1	US-08-920-827-18	Sequence 18, Appl
C 743	14	1.2	3943	4	US-08-956-653A-3	Sequence 3, Appl1	C 816	14	1.2	4954	1	US-08-921-177-18	Sequence 18, Appl
C 744	14	1.2	3943	5	PCT-US95-17025-3	Sequence 3, Appl1	C 817	14	1.2	4954	1	US-08-362-527C-18	Sequence 18, Appl
C 745	14	1.2	3987	1	US-07-688-352C-19	Sequence 19, Appl	C 818	14	1.2	4954	2	US-08-920-828-18	Sequence 18, Appl
C 746	14	1.2	3987	2	US-08-474-379C-19	Sequence 19, Appl	C 819	14	1.2	4959	4	US-09-670-618-14	Sequence 14, Appl
C 747	14	1.2	3987	3	US-09-146-249A-19	Sequence 19, Appl	C 820	14	1.2	4959	4	US-09-364-862-14	Sequence 14, Appl
C 748	14	1.2	3987	5	US-08-206-188B-19	Sequence 19, Appl	C 821	14	1.2	5027	3	US-08-680-506-2	Sequence 2, Appl1
C 749	14	1.2	3987	5	PCT-US91-02714-19	Sequence 19, Appl	C 822	14	1.2	5035	2	US-08-882-083-1	Sequence 2, Appl1
C 750	14	1.2	4002	2	US-08-331-488A-1	Sequence 1, Appl1	C 823	14	1.2	5035	2	US-08-558-107-1	Sequence 1, Appl1
C 751	14	1.2	4002	2	US-08-936-545-1	Sequence 1, Appl1	C 824	14	1.2	5035	2	US-09-243-539-1	Sequence 1, Appl1
C 752	14	1.2	4002	2	US-08-996-545-3	Sequence 3, Appl1	C 825	14	1.2	5236	5	PCT-US91-09422-16	Sequence 16, Appl
C 753	14	1.2	4002	4	US-09-328-320-1	Sequence 1, Appl1	C 826	14	1.2	5362	2	US-08-853-310-3	Sequence 3, Appl1
C 754	14	1.2	4002	4	US-09-328-320-1	Sequence 3, Appl1	C 827	14	1.2	5399	1	US-08-368-071-9	Sequence 9, Appl1
C 755	14	1.2	4003	4	US-09-087-465-1	Sequence 1, Appl1	C 828	14	1.2	5399	5	US-08-458-181-9	Sequence 9, Appl1
C 756	14	1.2	4042	4	US-08-406-030A-17	Sequence 17, Appl	C 829	14	1.2	5399	5	PCT-US93-02172-9	Sequence 9, Appl1
C 757	14	1.2	4068	2	US-08-474-379C-58	Sequence 58, Appl	C 830	14	1.2	5414	4	US-08-628-829-13	Sequence 13, Appl

831	14	1.2	5427	1	US-08-168-917-1	Sequence 1, Appl 1	904	14	1.2	7317	3	US-08-470-297A-2	Sequence 2, Appl 1
832	14	1.2	5427	2	US-08-460-510-1	Sequence 1, Appl 1	905	14	1.2	7317	5	PCT-US91-07149-2	Sequence 2, Appl 1
833	14	1.2	5427	2	US-08-460-490-1	Sequence 1, Appl 1	906	14	1.2	7320	1	US-08-440-787A-2	Sequence 2, Appl 1
834	14	1.2	5427	3	US-08-462-728-3	Sequence 1, Appl 1	907	14	1.2	7320	4	US-08-367-685-2	Sequence 2, Appl 1
835	14	1.2	5427	5	PCT-US92-00730-1	Sequence 1, Appl 1	908	14	1.2	7320	5	PCT-US91-07141-2	Sequence 2, Appl 1
836	14	1.2	5427	5	PCT-US92-00862-1	Sequence 1, Appl 1	909	14	1.2	7362	1	US-08-455-543A-7	Sequence 7, Appl 1
837	14	1.2	5433	3	US-08-929-329-1	Sequence 1, Appl 1	910	14	1.2	7362	1	US-08-193-078B-7	Sequence 7, Appl 1
838	14	1.2	5455	1	US-08-342-930-1	Sequence 1, Appl 1	911	14	1.2	7362	2	US-08-223-305C-7	Sequence 7, Appl 1
839	14	1.2	5467	2	US-07-745-206A-12	Sequence 12, Appl 1	912	14	1.2	7362	2	US-08-149-097D-7	Sequence 7, Appl 1
840	14	1.2	5467	2	US-08-311-363-6	Sequence 12, Appl 1	913	14	1.2	7362	3	US-08-450-565-7	Sequence 7, Appl 1
841	14	1.2	5499	1	US-07-695-564-4	Sequence 4, Appl 1	914	14	1.2	7362	3	US-08-984-709A-7	Sequence 7, Appl 1
842	14	1.2	5499	1	US-08-241-387-4	Sequence 4, Appl 1	915	14	1.2	7364	4	US-09-268-163-5	Sequence 5, Appl 1
843	14	1.2	5502	3	US-08-836-134-1	Sequence 1, Appl 1	916	14	1.2	7364	4	US-09-268-163-5	Sequence 5, Appl 1
844	14	1.2	5629	1	US-07-695-564-2	Sequence 2, Appl 1	917	14	1.2	7394	4	US-08-440-787A-6	Sequence 6, Appl 1
845	14	1.2	5629	1	US-08-241-387-2	Sequence 2, Appl 1	918	14	1.2	7394	4	US-08-464-136-1	Sequence 6, Appl 1
846	14	1.2	5820	4	US-09-029-213B-7	Sequence 7, Appl 1	919	14	1.2	7394	5	PCT-US91-07141-6	Sequence 6, Appl 1
847	14	1.2	5904	1	US-07-745-206A-6	Sequence 6, Appl 1	920	14	1.2	7409	1	US-08-440-787A-4	Sequence 6, Appl 1
848	14	1.2	5904	1	US-08-455-543A-3	Sequence 3, Appl 1	921	14	1.2	7409	1	US-08-367-685-4	Sequence 6, Appl 1
849	14	1.2	5904	2	US-08-193-078B-3	Sequence 3, Appl 1	922	14	1.2	7409	5	PCT-US91-07141-3	Sequence 6, Appl 1
850	14	1.2	5904	2	US-08-223-305C-3	Sequence 3, Appl 1	923	14	1.2	7445	4	US-08-464-136-1	Sequence 6, Appl 1
851	14	1.2	5904	2	US-08-311-363-6	Sequence 3, Appl 1	924	14	1.2	7445	1	US-08-440-787A-3	Sequence 6, Appl 1
852	14	1.2	5904	2	US-08-149-097D-3	Sequence 6, Appl 1	925	14	1.2	7445	2	US-08-349-131-1	Sequence 6, Appl 1
853	14	1.2	6152	1	US-08-557-139-1	Sequence 3, Appl 1	926	14	1.2	7445	2	US-08-470-297A-1	Sequence 6, Appl 1
854	14	1.2	6203	4	US-09-134-218-3	Sequence 11, Appl 1	927	14	1.2	7445	3	US-08-367-685-3	Sequence 6, Appl 1
855	14	1.2	6232	4	US-08-456-200B-11	Sequence 4, Appl 1	928	14	1.2	7445	5	PCT-US91-07141-3	Sequence 6, Appl 1
856	14	1.2	6291	3	US-08-817-188-4	Sequence 5, Appl 1	929	14	1.2	7445	5	PCT-US91-07141-3	Sequence 6, Appl 1
857	14	1.2	6376	1	US-08-104-073-5	Sequence 1, Appl 1	930	14	1.2	7502	3	US-08-969-644-6	Sequence 6, Appl 1
858	14	1.2	6529	4	US-08-789-329C-1	Sequence 3, Appl 1	931	14	1.2	7502	3	US-08-444-189-6	Sequence 6, Appl 1
859	14	1.2	6575	3	US-08-949-386-3	Sequence 3, Appl 1	932	14	1.2	7502	3	US-08-444-189-6	Sequence 6, Appl 1
860	14	1.2	6575	3	US-08-450-565-3	Sequence 3, Appl 1	933	14	1.2	7502	4	US-08-468-544-6	Sequence 6, Appl 1
861	14	1.2	6575	4	US-08-984-709A-3	Sequence 3, Appl 1	934	14	1.2	7502	4	US-08-464-136-4	Sequence 6, Appl 1
862	14	1.2	6639	1	US-08-727-034-1	Sequence 1, Appl 1	935	14	1.2	7557	2	US-08-349-131-4	Sequence 6, Appl 1
863	14	1.2	6642	2	US-08-727-034-5	Sequence 5, Appl 1	936	14	1.2	7557	5	PCT-US91-07149-4	Sequence 6, Appl 1
864	14	1.2	6642	2	US-08-380-403A-4	Sequence 4, Appl 1	937	14	1.2	7557	5	PCT-US91-07149-4	Sequence 6, Appl 1
865	14	1.2	6645	2	US-08-895-628-4	Sequence 4, Appl 1	938	14	1.2	7573	1	US-08-287-959-2	Sequence 6, Appl 1
866	14	1.2	6693	2	US-08-147-777-2	Sequence 2, Appl 1	939	14	1.2	7635	1	US-08-455-543A-1	Sequence 6, Appl 1
867	14	1.2	6693	3	US-08-452-872-2	Sequence 2, Appl 1	940	14	1.2	7635	1	US-08-455-543A-23	Sequence 6, Appl 1
868	14	1.2	6725	3	PCT-US93-03985-2	Sequence 36, Appl 1	941	14	1.2	7635	2	US-08-193-078B-1	Sequence 6, Appl 1
869	14	1.2	6725	3	US-08-949-386-36	Sequence 36, Appl 1	942	14	1.2	7635	2	US-08-193-078B-1	Sequence 6, Appl 1
870	14	1.2	6725	3	US-08-450-562-36	Sequence 36, Appl 1	943	14	1.2	7635	2	US-08-223-305C-1	Sequence 6, Appl 1
871	14	1.2	6725	4	US-08-984-709A-36	Sequence 36, Appl 1	944	14	1.2	7635	2	US-08-223-305C-23	Sequence 6, Appl 1
872	14	1.2	6743	3	US-08-932-280-1	Sequence 1, Appl 1	945	14	1.2	7635	2	US-08-149-097D-1	Sequence 6, Appl 1
873	14	1.2	6843	1	US-08-727-034-6	Sequence 6, Appl 1	946	14	1.2	7635	3	US-08-949-386-1	Sequence 6, Appl 1
874	14	1.2	6854	1	US-08-468-036-4	Sequence 4, Appl 1	947	14	1.2	7635	3	US-08-450-562-1	Sequence 6, Appl 1
875	14	1.2	6854	2	US-08-376-843-4	Sequence 4, Appl 1	948	14	1.2	7635	4	US-08-867-941-1	Sequence 6, Appl 1
876	14	1.2	6946	1	US-09-316-080-1	Sequence 1, Appl 1	949	14	1.2	7641	2	US-08-867-941-6	Sequence 6, Appl 1
877	14	1.2	6961	1	US-08-727-034-2	Sequence 2, Appl 1	950	14	1.2	7641	2	US-08-867-941-6	Sequence 6, Appl 1
878	14	1.2	6969	1	US-08-276-594A-1	Sequence 1, Appl 1	951	14	1.2	7641	4	US-09-074-658-6	Sequence 6, Appl 1
879	14	1.2	7011	4	US-09-268-163-9	Sequence 9, Appl 1	952	14	1.2	7641	4	US-09-074-658-6	Sequence 6, Appl 1
880	14	1.2	7032	4	US-09-324-867-1	Sequence 1, Appl 1	953	14	1.2	7650	2	US-08-867-941-1	Sequence 6, Appl 1
881	14	1.2	7056	1	US-08-121-202-1	Sequence 1, Appl 1	954	14	1.2	7650	2	US-08-867-941-1	Sequence 6, Appl 1
882	14	1.2	7083	4	US-09-198-839-1	Sequence 1, Appl 1	955	14	1.2	7650	4	US-09-074-658-1	Sequence 6, Appl 1
883	14	1.2	7125	1	US-07-745-206A-1	Sequence 1, Appl 1	956	14	1.2	7650	4	US-09-074-658-1	Sequence 6, Appl 1
884	14	1.2	7125	2	US-08-311-363-1	Sequence 1, Appl 1	957	14	1.2	7652	1	US-07-590-988A-1	Sequence 6, Appl 1
885	14	1.2	7143	4	US-09-381-862-4	Sequence 4, Appl 1	958	14	1.2	7680	4	US-09-210-748A-3	Sequence 6, Appl 1
886	14	1.2	7143	4	US-08-455-543A-8	Sequence 8, Appl 1	959	14	1.2	7729	2	US-08-464-136-3	Sequence 6, Appl 1
887	14	1.2	7175	2	US-08-193-078B-8	Sequence 8, Appl 1	960	14	1.2	7729	2	US-08-349-131-3	Sequence 6, Appl 1
888	14	1.2	7175	2	US-08-223-305C-8	Sequence 8, Appl 1	961	14	1.2	7729	2	US-08-470-297A-3	Sequence 6, Appl 1
889	14	1.2	7175	2	US-08-149-097D-8	Sequence 8, Appl 1	962	14	1.2	7729	5	PCT-US91-07149-3	Sequence 6, Appl 1
890	14	1.2	7175	3	US-08-949-386-8	Sequence 8, Appl 1	963	14	1.2	8056	3	US-09-136-605-14	Sequence 6, Appl 1
891	14	1.2	7175	3	US-08-450-562-8	Sequence 8, Appl 1	964	14	1.2	8056	3	US-08-306-691B-41	Sequence 6, Appl 1
892	14	1.2	7175	4	US-08-984-709A-8	Sequence 8, Appl 1	965	14	1.2	8082	1	US-08-187-785-1	Sequence 6, Appl 1
893	14	1.2	7177	4	US-09-268-163-7	Sequence 7, Appl 1	966	14	1.2	8082	5	PCT-US93-06251-28	Sequence 28, Appl 1
894	14	1.2	7266	3	US-08-713-118-1	Sequence 1, Appl 1	967	14	1.2	8118	2	US-08-464-136-5	Sequence 5, Appl 1
895	14	1.2	7266	3	US-09-453-007-1	Sequence 1, Appl 1	968	14	1.2	8118	2	US-08-349-131-5	Sequence 5, Appl 1
896	14	1.2	7294	1	US-08-440-787A-1	Sequence 1, Appl 1	969	14	1.2	8118	3	US-08-470-297A-5	Sequence 5, Appl 1
897	14	1.2	7294	1	US-08-440-787A-5	Sequence 5, Appl 1	970	14	1.2	8241	6	PCT-US91-07149-5	Sequence 6, Appl 1
898	14	1.2	7294	4	US-08-367-685-1	Sequence 1, Appl 1	971	14	1.2	8241	6	PCT-US91-07149-5	Sequence 6, Appl 1
899	14	1.2	7294	4	US-08-367-685-5	Sequence 5, Appl 1	972	14	1.2	8241	6	PCT-US91-07149-5	Sequence 6, Appl 1
900	14	1.2	7294	5	PCT-US91-07141-1	Sequence 1, Appl 1	973	14	1.2	8299	3	US-08-462-014-2	Sequence 3, Appl 1
901	14	1.2	7294	5	PCT-US91-07141-5	Sequence 5, Appl 1	974	14	1.2	8299	4	US-08-923-137-3	Sequence 3, Appl 1
902	14	1.2	7317	1	US-08-464-136-2	Sequence 2, Appl 1	975	14	1.2	8299	4	US-08-923-137-3	Sequence 3, Appl 1
903	14	1.2	7317	2	US-08-349-131-2	Sequence 2, Appl 1	976	14	1.2	8321	3	US-08-563-869A-5	Sequence 5, Appl 1
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978 14 1.2 8509 1 US-08-462-014-1 Sequence 1, Appli
979 14 1.2 8509 4 US-08-973-334-4 Sequence 4, Appli
980 14 1.2 8509 4 US-09-563-869A-4 Sequence 4, Appli
981 14 1.2 8640 1 US-08-570-311-28 Sequence 28, Appli
982 14 1.2 8967 1 US-08-366-851A-1 Sequence 1, Appli
983 14 1.2 9009 1 US-07-864-004B-3 Sequence 3, Appli
984 14 1.2 9009 1 US-08-251-937A-3 Sequence 3, Appli
985 14 1.2 9009 1 US-08-212-133A-1 Sequence 1, Appli
986 14 1.2 9009 1 US-08-474-503-1 Sequence 1, Appli
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988 14 1.2 9009 4 US-09-037-601-1 Sequence 1, Appli
989 14 1.2 9009 5 PCT-US93-03275-3 Sequence 3, Appli
990 14 1.2 9009 5 PCT-US94-13200-1 Sequence 1, Appli
991 14 1.2 9046 1 US-08-227-536-1 Sequence 1, Appli
992 14 1.2 9046 5 PCT-US95-04682-1 Sequence 1, Appli
993 14 1.2 9354 1 US-08-683-839B-2 Sequence 2, Appli
994 14 1.2 9370 1 US-08-320-559-27 Sequence 27, Appli
995 14 1.2 9370 3 US-08-545-860D-27 Sequence 27, Appli
996 14 1.2 9370 5 PCT-US94-04496-27 Sequence 27, Appli
997 14 1.2 9391 1 US-08-320-559-25 Sequence 25, Appli
998 14 1.2 9391 3 US-08-545-860D-25 Sequence 25, Appli
999 14 1.2 9391 5 PCT-US94-04496-25 Sequence 25, Appli
1000 14 1.2 9723 1 US-08-083-590A-21 Sequence 21, Appli

ALIGNMENTS

RESULT 1
US-08-451-822A-15/c
; Sequence 15, Application US/08451822A
; Patent No. 5863888
; GENERAL INFORMATION:
; APPLICANT: Dionne, Craig A
; APPLICANT: Crumley, Greg
; APPLICANT: Jaye, Michael C
; APPLICANT: Schlessinger, Joseph
; TITLE OF INVENTION: Fibroblast Growth Factor Receptors
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Legal Department
; STREET: 500 Arcola Road
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/451, 822A
; FILING DATE: 26-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/323,430
; FILING DATE: 14-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/934,372
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/549,587
; FILING DATE: 06-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Savitzky, Martin
; REGISTRATION NUMBER: 29,699
; REFERENCE/DOCKET NUMBER: A0496E
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-3816
; TELEFAX: (610) 454-3808
; INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:
LENGTH: 3416 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-451-822A-15

Query Match 1.6%; Score 18; DB 2; Length 3416;
Best Local Similarity 100.0%; Pred. No. 9.8;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 38 gtctgctgtgtctgtcgc 55
Db 3347 gtctgctgtgtctgtcgc 3330

RESULT 2
US-08-323-430-15/c
; Sequence 15, Application US/08323430
; Patent No. 6344546
; GENERAL INFORMATION:
; APPLICANT: Dionne, Craig A
; APPLICANT: Crumley, Greg
; APPLICANT: Jaye, Michael C
; APPLICANT: Schlessinger, Joseph
; TITLE OF INVENTION: Fibroblast Growth Factor Receptors
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Legal Department
; STREET: 500 Arcola Road
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/323,430
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US to be assigned
; FILING DATE: 21-AUG-1992
; APPLICATION NUMBER: US 07/549,587
; FILING DATE: 06-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Goodman, Rosanne
; REGISTRATION NUMBER: 32,534
; REFERENCE/DOCKET NUMBER: A0496
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 454-3817
; TELEFAX: (215) 454-3808
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3416 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-323-430-15

Query Match 1.6%; Score 18; DB 4; Length 3416;
Best Local Similarity 100.0%; Pred. No. 9.8;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 38 gtctgctgtgtctgtcgc 55
|||||

Best Local Similarity 100.0%; Pred. No. 32;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 797 tgatgaacaacctgaag 813
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DB 2333 TGATGAACAACCTGAAA 2317

RESULT 6
US-09-265-315-65/c
; Sequence 65, Application US/09265315
; Patent No. 6187541
; GENERAL INFORMATION:
; APPLICANT: Benton, Bret
; APPLICANT: Lee, Ying J.
; APPLICANT: Malouin, Francois
; APPLICANT: Martin, Patrick K.
; APPLICANT: Schmidt, Molly B.
; APPLICANT: Sun, Dongxu
; TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
; TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS
; NUMBER OF SEQUENCES: 111
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/265,315
; FILING DATE: March 9, 1999
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/714,918
; FILING DATE: September 13, 1996
; APPLICATION NUMBER: 60/009,102
; FILING DATE: December 22, 1995
; APPLICATION NUMBER: 60/003,798
; FILING DATE: September 15, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 240/247
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEFAX: 67-3510
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2976 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-265-315-65

Query Match 1.5%; Score 17; DB 4; Length 2976;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 797 tgatgaacaacctgaag 813
|||||
DB 2333 TGATGAACAACCTGAAA 2317

RESULT 7
US-09-265-315-65/c
; Sequence 65, Application US/09265315
; Patent No. 6187541
; GENERAL INFORMATION:
; APPLICANT: Benton, Bret
; APPLICANT: Lee, Ying J.
; APPLICANT: Malouin, Francois
; APPLICANT: Martin, Patrick K.
; APPLICANT: Schmidt, Molly B.
; APPLICANT: Sun, Dongxu
; TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
; TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS
; NUMBER OF SEQUENCES: 111
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/265,315
; FILING DATE: March 9, 1999
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/714,918
; FILING DATE: September 13, 1996
; APPLICATION NUMBER: 60/009,102
; FILING DATE: December 22, 1995
; APPLICATION NUMBER: 60/003,798
; FILING DATE: September 15, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 240/247
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEFAX: 67-3510
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2976 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-265-315-65

Query Match 1.5%; Score 17; DB 4; Length 2976;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 797 tgatgaacaacctgaag 813
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DB 2333 TGATGAACAACCTGAAA 2317

RESULT 8
US-09-266-417-65/c
; Sequence 65, Application US/09266417
; Patent No. 628588
; GENERAL INFORMATION:
; APPLICANT: Benton, Bret

APPLICANT: Lee, Ving J.
APPLICANT: Malouin, Francois
APPLICANT: Martin, Patrick K.
APPLICANT: Schmid, Molly B.
APPLICANT: Sun, Dongxu
TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS
TITLE OF INVENTION: TARGET GENES
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/266,417
FILING DATE: March 9, 1999
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/714, 918
FILING DATE: September 13, 1996
APPLICATION NUMBER: 60/009,102
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 240/248
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 2976 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-266-417-65

Query Match 1.5%; Score 17; DB 4; Length 2976;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 797 tgatgaacaactgaa 813
|||||
DB 2333 TGATGAACACCTGAAA 2317

RESULT 9
US-08-070-301-2
Sequence 2, Application US/08070301
Patent No. 5871995
GENERAL INFORMATION:
APPLICANT: IIDA, Toshio
APPLICANT: KAMINUMA, Toshihiko
APPLICANT: FUSE, Yuka
APPLICANT: TAJIMA, Masahiro
APPLICANT: YAMAGI, Mitsuo
APPLICANT: OKAMOTO, Hitoshi
APPLICANT: KISHIMOTO, Jiro
APPLICANT: IFUKU, Ohji

APPLICANT: KATO, Ichiro
TITLE OF INVENTION: ENZYME PARTICIPATING IN C-TERMINAL
TITLE OF INVENTION: AMIDATION, AND METHOD OF PREPARING SAME AND USE THEREOF
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wegner, Cantor, Mueller & Player, P.C.
STREET: 1233 20th Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20036-8218
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/070,301
FILING DATE: 24-MAY-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 1-209687
FILING DATE: 15-AUG-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 1-181933
FILING DATE: 31-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-76331
FILING DATE: 26-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-106412
FILING DATE: 24-APR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-205475
FILING DATE: 02-AUG-1990
ATTORNEY/AGENT INFORMATION:
NAME: Player, William E.
REGISTRATION NUMBER: 31,409
REFERENCE/DOCKET NUMBER: P-450-22830
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-040
TELEFAX: (202) 835-0605
TELEX: 440706
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 6638 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Horse
FEATURE:
NAME/KEY: CDS
LOCATION: 11..3070
US-08-070-301-2

Query Match 1.5%; Score 17; DB 2; Length 6638;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 318 gattgcctgagatata 334
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DB 1514 GATTGCCTGGAGATATA 1530

RESULT 10
US-08-846-111D-15/C
Sequence 15, Application US/08846111D
Patent No. 6017705
GENERAL INFORMATION:
APPLICANT: Lurquin, Christophe; Brasseur, Francis;

APPLICANT: Boon-Falleur, Thierry
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Which Are
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
ZIP: 10022-7513
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect For Dos 6.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/846.111D
FILING DATE: 25-APRIL-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/658,578
FILING DATE: 5-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/403,388
FILING DATE: 14-MARCH-1995
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 6017705man D.
REGISTRATION/DOCKET NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5444.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 40352 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-846-111D-15

Query Match 1.5%; Score 17; DB 3; Length 40352;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 200 acaactgaagacctg 216
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Db 13873 ACAACCTGAAGACCTG 13857

RESULT 11
US-08-920-422-17/c
Sequence 17, Application US/08920422A
Patent No. 6255473
GENERAL INFORMATION:
APPLICANT: Vitek, Michael P.
APPLICANT: Mitsuda, No. 6255473iak1
APPLICANT: Roses, Allen D.
TITLE OF INVENTION: Presentin-1 Gene Promoter
FILE REFERENCE: VITEKPRESENTIN
CURRENT APPLICATION NUMBER: US/08/920.422A
NUMBER OF SEQ ID NOS: 22
FILING DATE: 1997-08-29
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 17
LENGTH: 48974
TYPE: DNA
ORGANISM: Mus musculus
US-08-920-422-17

Query Match 1.5%; Score 17; DB 4; Length 48974;
Best Local Similarity 100.0%; Pred. No. 31;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1016 taaactgaagacctg 1032
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Db 34191 TAAACTGAAGACCTG 34175

RESULT 12
US-09-651-656-2/c
Sequence 2, Application US/09651656
Patent No. 6340566
GENERAL INFORMATION:
APPLICANT: MCCUTHEN-MALONEY, SANDRA
TITLE OF INVENTION: LAWRENCE LIVERMORE NATIONAL LABORATORY
TITLE OF INVENTION: DETECTION AND QUANTITATION OF SINGLE NUCLEOTIDE
TITLE OF INVENTION: POLYMORPHISMS, DNA SEQUENCE VARIATIONS, DNA ROTATIONS,
FILE REFERENCE: IL-10689
CURRENT APPLICATION NUMBER: US/09/651.656
CURRENT FILING DATE: 2000-08-29
PRIOR APPLICATION NUMBER: 60/192,764
PRIOR FILING DATE: 2000-03-28
NUMBER OF SEQ ID NOS: 106
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 723
TYPE: DNA
ORGANISM: Homo sapiens
US-09-651-656-2

Query Match 1.4%; Score 16; DB 4; Length 723;
Best Local Similarity 100.0%; Pred. No. 16+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 281 aatcatcgtagctag 296
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Db 371 AATCATCGTAGCTAG 356

RESULT 13
US-08-982-956-2
Sequence 2, Application US/08982956
Patent No. 5861312
GENERAL INFORMATION:
APPLICANT: Varshevsky, Alexander
APPLICANT: Kwon, Yong Tae
TITLE OF INVENTION: NUCLEIC ACID ENCODING MAMMALIAN DBRI
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Kevin M. Farrell, P.C.
STREET: P.O. Box 999
CITY: York Harbor
STATE: ME
COUNTRY: US
ZIP: 03911
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/982.956
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Farrell, Kevin M.
REGISTRATION NUMBER: 35,505
REFERENCE/DOCKET NUMBER: CIT-2001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (207) 363-0558
TELEFAX: (207) 363-0528
INFORMATION FOR SEQ ID NO: 2:

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SEQUENCE CHARACTERISTICS:
LENGTH: 1001 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..999
US-08-982-956-2

Query Match          1.4%; Score 16; DB 2; Length 1001;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 548 atgataaagaagaac 563
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DB 932 ATGATTAAGAAAAAGC 947

RESULT 14
US-09-228-317-2
Sequence 2, Application US/09228317
Patent No. 6159732
GENERAL INFORMATION:
APPLICANT: Vaishavsky, Alexander
APPLICANT: Kwon, Yong Tae
TITLE OF INVENTION: NUCLEIC ACID ENCODING MAMMALIAN UBRL
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSER: Kevin M. Farrell, P.C.
STREET: P.O. Box 999
CITY: York Harbor
STATE: ME
COUNTRY: US
ZIP: 03911
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/228,317
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Farrell, Kevin M.
REGISTRATION NUMBER: 35,505
REFERENCE/DOCKET NUMBER: CIT-2001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (207) 363-0558
TELEFAX: (207) 363-0528
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1001 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..999
US-09-228-317-2

Query Match          1.4%; Score 16; DB 3; Length 1001;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 548 atgataaagaagaac 563
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DB 932 ATGATTAAGAAAAAGC 947
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RESULT 15
US-08-176-427B-9
Sequence 9, Application US/08176427B
Patent No. 5789543
GENERAL INFORMATION:
APPLICANT: Ingham, Phillip W.
APPLICANT: McMahon, Andrew P.
APPLICANT: Tablo, Clifford J.
TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSER: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/176,427B
FILING DATE: 30-DEC-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HMI-006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1256 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1257
US-08-176-427B-9

Query Match          1.4%; Score 16; DB 1; Length 1256;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 206 tgaaggaactgaacc 221
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DB 644 TGAAGGACCTGAACCC 659
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Search completed: May 7, 2002, 18:11:29
Job time: 8135 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 7, 2002, 15:09:30 ; Search time 1802.55 Seconds
(without alignments)
8513.516 Million cell updates/sec

Title: US-09-579-383-1
Perfect score: 1137
Sequence: 1 atgaatttaccgtaataa.....tcgttgaagcctgcactaa 1137

Scoring table: OLIGO NUC
Gap60 60.0 , Gapext 60.0

Searched: 13736207 seqs, 6748477542 residues

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Minimum DB seq length: 0
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Post-processing: Listing first 1000 summaries

Database :

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16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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C 6	20	1.8	339	9	AA269349
C 7	20	1.8	370	9	A1834906
C 8	20	1.8	373	9	AA590068
C 9	20	1.8	376	10	W30259
C 10	20	1.8	383	9	AM822056
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C 13	20	1.8	413	10	BF783504
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C 22	20	1.8	510	10	B1320819
C 23	20	1.8	512	12	TA196A01P
C 24	20	1.8	531	9	AA881704
C 25	20	1.8	545	12	A0358119
C 26	20	1.8	549	12	A0653019
C 27	20	1.8	553	12	A0943352
C 28	20	1.8	556	12	TA332B01P
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C 54	19	1.7	234	9	AV239268
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C 57	19	1.7	359	10	H92777
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BG969104	602835078
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AK002424	Mus muscu
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BF787117	602108654
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BB143865	BB143865
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AU240425	AU240425
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AV540025	AV540025
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AG085862	Pan trogl
AV405606	AV405606
AL594699	AL594699
BB441046	BB441046
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AG129762	Pan trogl
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C 94	19	1.7	832	12	AZ535507	AZ535507 ENTC068TF	C 167	18	1.6	610	10	BI387135	BI387135 RE43523.5
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C 97	19	1.7	1003	12	CNS024Z7	AL181420 Tetradon	C 170	18	1.6	612	9	AW949428	AW949428 EST361498
C 98	18	1.6	207	10	BI006414	BI006414 MRL-RT003	C 171	18	1.6	617	9	AW949426	AW949426 EST361496
C 99	18	1.6	253	10	BG191540	BG191540 RST10634	C 172	18	1.6	621	12	AZ818350	AZ818350 2M0088N18
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C 102	18	1.6	281	10	BE500504	BE500504 WHE0987-0	C 175	18	1.6	625	9	BE660052	BE660052 856 Gmax
C 103	18	1.6	315	9	AJ280504	AJ280504 4A3A-AAO-	C 176	18	1.6	629	9	AV651738	AV651738 AV651738
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C 106	18	1.6	380	10	BI622807	BI622807 RH54730.5	C 179	18	1.6	636	10	BE712434	BE712434 QV2-HT069
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C 108	18	1.6	390	9	AA490022	AA490022 ab02b04.s	C 181	18	1.6	638	12	AZ343817	AZ343817 IM0077E03
C 109	18	1.6	392	12	AQ486017	AQ486017 RPCI-11-2	C 182	18	1.6	642	9	AW305549	AW305549 f160612.y
C 110	18	1.6	395	9	BB800724	BB800724 BB800724	C 183	18	1.6	643	10	BG086723	BG086723 LERAD35TF
C 111	18	1.6	400	9	AA614441	AA614441 BP230005A	C 184	18	1.6	646	12	AQ955332	AQ955332 2M0221G13
C 112	18	1.6	402	10	R70205	R70205 v180b12.r1	C 185	18	1.6	646	12	AZ955245	AZ955245 2M0221G13
C 113	18	1.6	403	9	AA834917	AA834917 aj37e12.s	C 186	18	1.6	651	12	AG133350	AG133350 Pan LT091
C 114	18	1.6	409	10	BE620895	BE620895 601483747	C 187	18	1.6	653	10	BI163572	BI163572 RE03006.5
C 115	18	1.6	412	9	AW159225	AW159225 za62e02.x	C 188	18	1.6	664	9	AV681532	AV681532 AV681532
C 116	18	1.6	415	9	AW429933	AW429933 68542 MAR	C 189	18	1.6	672	10	BG706936	BG706936 602672123
C 117	18	1.6	417	9	AW830988	AW830988 sm21a03.Y	C 190	18	1.6	713	9	AV726725	AV726725 AV726725
C 118	18	1.6	427	12	AZ487275	AZ487275 IM0316117	C 191	18	1.6	717	12	BH244864	BH244864 AUTJA78TF
C 119	18	1.6	431	12	BH255971	BH255971 RPH10BAM0	C 192	18	1.6	729	9	AI906341	AI906341 IL-BT108-
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C 121	18	1.6	440	10	BE863083	BE863083 UT-M-BHO-	C 194	18	1.6	736	10	BF786714	BF786714 602111477
C 122	18	1.6	442	9	AA235910	AA235910 z543c12.r	C 195	18	1.6	766	12	AZ416858	AZ416858 IM0192116
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C 125	18	1.6	448	9	AV440616	AV440616 AV440616	C 198	18	1.6	810	12	AQ606085	AQ606085 nbebd015F
C 126	18	1.6	450	12	AZ331087	AZ331087 IM0056D16	C 199	18	1.6	812	12	BH092880	BH092880 RPCI-24-3
C 127	18	1.6	453	12	AQ802835	AQ802835 HS_3186-A	C 200	18	1.6	817	9	AF074799	AF074799 AF074799
C 128	18	1.6	454	12	AQ060044	AQ060044 CIT-HSP-2	C 201	18	1.6	817	10	BI660191	BI660191 603302567
C 129	18	1.6	455	12	AQ481220	AQ481220 RPCI-11-2	C 202	18	1.6	822	12	AQ955331	AQ955331 LERAD35TF
C 130	18	1.6	477	12	B43843	B43843 HS-1058-A2-	C 203	18	1.6	825	12	CNS04KGI	AL294795 Tetradon
C 131	18	1.6	479	9	AV596685	AV596685 AV596685	C 204	18	1.6	832	9	AF074804	AF074804 AF074804
C 132	18	1.6	482	10	BF769079	BF769079 QV3-TT000	C 205	18	1.6	834	10	BI765848	BI765848 603049874
C 133	18	1.6	487	9	AA664355	AA664355 at25h05.s	C 206	18	1.6	834	12	AQ744814	AQ744814 HS_5506-A
C 134	18	1.6	488	9	AW193590	AW193590 xM09h10.x	C 207	18	1.6	844	12	CNS0454G	AL274921 Tetradon
C 135	18	1.6	509	12	BG673531	BG673531 DRNCFH09	C 208	18	1.6	858	9	AI403531	AI403531 G822991..5
C 136	18	1.6	522	10	BH442152	BH442152 BOHWH64TF	C 209	18	1.6	872	12	BH131071	BH131071 ENTNML2TF
C 137	18	1.6	507	10	BG511299	BG511299 s8d1b02.	C 210	18	1.6	879	12	AZ693029	AZ693029 ENTL0944TF
C 138	18	1.6	515	10	BE329989	BE329989 s8g72a11.y	C 211	18	1.6	935	10	BE549386	BE549386 601075773
C 139	18	1.6	517	10	BE721156	BE721156 188212 MA	C 212	18	1.6	937	12	CNS043D8	AL272645 Tetradon
C 140	18	1.6	519	12	AQ688657	AQ688657 nDxb0078E	C 213	18	1.6	941	10	BF532233	BF532233 6020773134
C 141	18	1.6	519	12	AZ288853	AZ288853 RPCI-23-1	C 214	18	1.6	997	12	CNS04RL1	AL303323 Tetradon
C 142	18	1.6	520	12	BH198866	BH198866 TC3-69F21	C 215	18	1.6	1006	10	BI086478	BI086478 602849748
C 143	18	1.6	522	10	BG553721	BG553721 daC27a11.	C 216	18	1.6	1036	10	BG390165	BG390165 602415687
C 144	18	1.6	524	10	BF018702	BF018702 ux97b02.x	C 217	18	1.6	1085	10	BI410118	BI410118 602964050
C 145	18	1.6	524	12	AQ824284	AQ824284 HS_3249-B	C 218	18	1.6	1190	10	BG844746	BG844746 1024007F0
C 146	18	1.6	528	9	AI042703	AI042703 uc76f07.x	C 219	18	1.6	1325	10	BI331809	BI331809 602982380
C 147	18	1.6	529	10	BI608157	BI608157 RML2334.5	C 220	18	1.6	2219	11	AK011270	AK011270 Mus muscu
C 148	18	1.6	532	12	AQ080825	AQ080825 HS_5258.B	C 221	18	1.6	3952	11	AK014555	AK014555 Mus muscu
C 149	18	1.6	539	9	AJ280428	AJ280428 4A3A-AAP-	C 222	17	1.5	81	9	AA897476	AA897476 a148e11.s
C 150	18	1.6	540	12	AZ145902	AZ145902 SP_0015-B	C 223	17	1.5	87	12	AZ776811	AZ776811 2M0010113
C 151	18	1.6	542	12	AZ067610	AZ067610 RPCI-23-4	C 224	17	1.5	146	9	AV174887	AV174887 AV174887
C 152	18	1.6	543	9	BE124087	BE124087 EST394212	C 225	17	1.5	154	10	T20190	T20190 D165F Heart
C 153	18	1.6	544	9	AI041534	AI041534 oV82b07.x	C 226	17	1.5	157	9	AW318923	AW318923 UN09607.y
C 154	18	1.6	546	12	AQ083267	AQ083267 HS_5503.B	C 227	17	1.5	174	12	AQ276846	AQ276846 CITBI-EL-
C 155	18	1.6	549	9	AA183718	AA183718 mC33h06.r	C 228	17	1.5	178	10	BM166184	BM166184 EST368707
C 156	18	1.6	552	9	AJ281632	AJ281632 4A3A-P8C6	C 229	17	1.5	186	12	B37915	B37915 HS_1046-A2-
C 157	18	1.6	555	10	BI615400	BI615400 RH45015.5	C 230	17	1.5	191	9	AV624058	AV624058 AV624058
C 158	18	1.6	555	10	BI615400	BI615400 RH45015.5	C 231	17	1.5	198	9	BB405044	BB405044 BB405044
C 159	18	1.6	562	9	AB658268	AB658268 fc20g10.y	C 232	17	1.5	207	10	BM421440	BM421440 V014D07 O
C 160	18	1.6	563	9	BB695595	BB695595 BB695595	C 233	17	1.5	212	9	AV263336	AV263336 AV263336
C 161	18	1.6	567	12	BH554683	BH554683 BOHTE62TF	C 234	17	1.5	212	10	BG602891	BG602891 EST501981
C 162	18	1.6	575	9	AA141048	AA141048 CK01116.C	C 235	17	1.5	215	9	BB035921	BB035921 BB035921
C 163	18	1.6	575	12	AQ734966	AQ734966 HS_3085_B	C 236	17	1.5	216	9	BB214004	BB214004 BB214004

C 237	17	1.5	219	9	AV087749	AV087749	310	17	1.5	361	10	T26683	T26683 T047 MVT4
C 238	17	1.5	219	9	BB073298	BB073298	311	17	1.5	362	9	AW227209	AW227209 um67e07.y
C 239	17	1.5	232	10	BG626388	CC-est1cL	312	17	1.5	366	9	AJ283431	AJ283431 AA3B-AAB-
C 240	17	1.5	233	9	AV369395	AV369395	313	17	1.5	367	9	AI810136	AI810136 wf65h09.x
C 241	17	1.5	236	9	BB212611	BB212611	314	17	1.5	368	10	BE864213	BE864213 UI-M-BH1-
C 242	17	1.5	244	9	AV246831	AV246831	315	17	1.5	369	12	BH220676	BH220676 1006096C0
C 243	17	1.5	245	9	BB019686	BB019686	316	17	1.5	373	9	AA318102	AA318102 EST20171
C 244	17	1.5	247	10	BI433041	BI433041	317	17	1.5	374	9	AV682452	AV682452 AV682452
C 245	17	1.5	250	10	BI754419	BI754419	318	17	1.5	377	10	BM246803	BM246803 K0743B06-
C 246	17	1.5	251	9	AV563105	AV563105	319	17	1.5	377	10	BE485174	BE485174 172102 BA
C 247	17	1.5	252	9	AV355936	AV355936	320	17	1.5	378	10	BI568421	BI568421 RH39864.5
C 248	17	1.5	253	9	AV869532	AV869532	321	17	1.5	379	10	D60823	D60823 HUM133B04A
C 249	17	1.5	257	9	BB608289	BB608289	322	17	1.5	380	9	AA451151	AA451151 vF88C03.r
C 250	17	1.5	263	12	BH014439	BH014439	323	17	1.5	380	9	BB800684	BB800684 BB800684
C 251	17	1.5	267	10	BE624836	BE624836	324	17	1.5	381	10	H96089	H96089 yv98e12..s1
C 252	17	1.5	269	9	BB083608	BB083608	325	17	1.5	383	10	BF766142	BF766142 IL2-CS007
C 253	17	1.5	270	9	AA893954	AA893954	326	17	1.5	384	9	AA889167	AA889167 ak25e06.s
C 254	17	1.5	271	9	AM086481	AM086481	327	17	1.5	384	10	BF787716	BF787716 MR1-KT005
C 255	17	1.5	273	9	AI563535	AI563535	328	17	1.5	385	9	AI998537	AI998537 701546087
C 256	17	1.5	274	9	AM319589	AM319589	329	17	1.5	385	10	BG603969	BG603969 EST503059
C 257	17	1.5	275	9	BB370551	BB370551	330	17	1.5	386	9	BB846189	BB846189 B846189
C 258	17	1.5	277	10	BI565449	BI565449	331	17	1.5	386	9	AI956576	AI956576 u178h12.y
C 259	17	1.5	278	9	BB150575	BB150575	332	17	1.5	389	12	AQ089359	AQ089359 HS_318B_B
C 260	17	1.5	279	9	BB484459	BB484459	333	17	1.5	390	9	AA682873	AA682873 z15h10.s
C 261	17	1.5	279	10	BF454095	BF454095	334	17	1.5	390	9	BB669162	BB669162 BB669162
C 262	17	1.5	280	9	AA795031	AA795031	335	17	1.5	390	10	BG668501	BG668501 DRNALD05
C 263	17	1.5	280	9	AV902947	AV902947	336	17	1.5	392	9	AJ280668	AJ280668 AA3A-AAS-
C 264	17	1.5	280	12	A2751102	A2751102	337	17	1.5	393	9	BE155508	BE155508 PM1-HT035
C 265	17	1.5	281	9	BB328252	BB328252	338	17	1.5	393	10	H60920	H60920 yf14d05.r1
C 266	17	1.5	285	9	AA486409	AA486409	339	17	1.5	394	12	A2939550	A2939550 2M0198N03
C 267	17	1.5	287	9	BB371042	BB371042	340	17	1.5	395	10	BM336214	BM336214 MEST191-A
C 268	17	1.5	290	9	BB080130	BB080130	341	17	1.5	396	12	AQ178354	AQ178354 HS_-2220_A
C 269	17	1.5	290	9	BB128545	BB128545	342	17	1.5	397	12	AQ136268	AQ136268 HS_-3056_B
C 270	17	1.5	294	10	BF748031	BF748031	343	17	1.5	398	10	BG726422	BG726422 sad44d12.
C 271	17	1.5	294	10	BF453154	BF453154	344	17	1.5	400	9	AA798061	AA798061 vW32e02.r
C 272	17	1.5	294	10	BF453154	BF453154	345	17	1.5	401	9	AV442183	AV442183 AV442183
C 273	17	1.5	296	10	BI051370	BI051370	346	17	1.5	401	9	BE155513	BE155513 PM1-HT035
C 274	17	1.5	297	9	BB282453	BB282453	347	17	1.5	402	10	BE481859	BE481859 167459 BA
C 275	17	1.5	297	12	AO396241	AO396241	348	17	1.5	404	9	AI103530	AI103530 EST212819
C 276	17	1.5	298	10	BF654372	BF654372	349	17	1.5	404	10	BF961960	BF961960 QV2--NN004
C 277	17	1.5	299	4	BB714885	BB714885	350	17	1.5	404	10	BF397186	BF397186 UI-R-BSD2-
C 278	17	1.5	300	9	AV183288	AV183288	351	17	1.5	405	10	NA3877	NA3877 y443f09.r1
C 279	17	1.5	300	9	AV333437	AV333437	352	17	1.5	406	9	AA031840	AA031840 zK17a03.r
C 280	17	1.5	300	9	BB103979	BB103979	353	17	1.5	406	9	AM259327	AM259327 um92a12.y
C 281	17	1.5	300	10	C33963	C33963	354	17	1.5	406	10	BM362465	BM362465 BS3200450
C 282	17	1.5	301	12	A0796342	A0796342	355	17	1.5	408	9	AA815125	AA815125 oc03e07.s
C 283	17	1.5	301	12	BE822824	BE822824	356	17	1.5	408	10	H63818	H63818 yf52e06.r1
C 284	17	1.5	305	10	BB530362	BB530362	357	17	1.5	408	12	AQ0563197	AQ0563197 HS_-5302_A
C 285	17	1.5	307	9	BB530362	BB530362	358	17	1.5	409	9	A1845514	A1845514 UI-M-AOI-
C 286	17	1.5	308	9	AW279061	AW279061	359	17	1.5	409	9	BB846348	BB846348 BB846348
C 287	17	1.5	308	9	BB103652	BB103652	360	17	1.5	412	9	AI758015	AI758015 EESTea06
C 288	17	1.5	309	9	AI109751	AI109751	361	17	1.5	412	9	BE155119	BE155119 PM1-HT035
C 289	17	1.5	309	9	BB098748	BB098748	362	17	1.5	412	12	AO277745	AO277745 CITBI-EI-
C 290	17	1.5	310	9	AA443706	AA443706	363	17	1.5	413	9	AA721835	AA721835 33141.fam
C 291	17	1.5	314	9	AA273869	AA273869	364	17	1.5	413	9	BB800943	BB800943 BB800943
C 292	17	1.5	316	9	AW798776	AW798776	365	17	1.5	415	12	A2762260	A2762260 1M0557105
C 293	17	1.5	322	10	BG642362	BG642362	366	17	1.5	416	9	BB726873	BB726873 BB726873
C 294	17	1.5	324	9	AA916439	AA916439	367	17	1.5	416	12	A2948878	A2948878 2M0212A07
C 295	17	1.5	328	10	D23882	D23882	368	17	1.5	419	9	AI098069	AI098069 uc28B05.x
C 296	17	1.5	329	9	BB259533	BB259533	369	17	1.5	420	9	BB677405	BB677405 BB677405
C 297	17	1.5	335	9	AM259857	AM259857	370	17	1.5	421	10	R91142	R91142 yp94c07.s1
C 298	17	1.5	336	10	BF150920	BF150920	371	17	1.5	423	12	AO613482	AO613482 HS_-5117_B
C 299	17	1.5	340	10	BG053436	RH12_8.H	372	17	1.5	423	9	BE148688	BE148688 MR0-HT024
C 300	17	1.5	342	9	AV543320	AV543320	373	17	1.5	423	12	AO363157	AO363157 ndx0055C
C 301	17	1.5	344	12	A2295518	A2295518	374	17	1.5	425	9	AM143640	AM143640 EST293935
C 302	17	1.5	345	9	AM015489	AM015489	375	17	1.5	425	9	AM919534	AM919534 EST350838
C 303	17	1.5	345	9	AM061528	AM061528	376	17	1.5	425	10	BG629869	BG629869 CC-est1cL
C 304	17	1.5	345	10	H54475	H54475	377	17	1.5	426	10	BE722840	BE722840 19123.MA
C 305	17	1.5	346	9	AA095474	AA095474	378	17	1.5	426	12	BH224002	BH224002 1006116C0
C 306	17	1.5	351	9	AJ280381	AJ280381	379	17	1.5	427	12	AO110563	AO110563 CIT-HSP-2
C 307	17	1.5	353	10	D60612	D60612	380	17	1.5	428	9	AO771689	AO771689 HS_-5412_A
C 308	17	1.5	360	9	AA690738	AA690738	381	17	1.5	430	12	AM502823	AM502823 UI-HF-BNO
C 309	17	1.5	360	10	C40260	C40260	382	17	1.5	430	10	BF738227	BF738227 CM3-KT003

C 383	17	1.5	431	10	BM116916	BM116916 L0843B08-	456	17	1.5	489	9	AI558774	AI558774 fB80d01.Y
C 384	17	1.5	431	10	BF229454	BF229454 RCO-C1003	C 457	17	1.5	491	10	BM330902	BM330902 PIC1_67A
C 385	17	1.5	431	10	BF662363	BF662363 mea84c02.	C 458	17	1.5	492	10	B1203452	B1203452 B1203452
C 386	17	1.5	432	9	BB800416	BB800416 BB800416	C 459	17	1.5	493	10	BC552737	BC552737 dab75c05.
C 387	17	1.5	432	10	BE327099	BE327099 PWO-BN006	C 460	17	1.5	494	9	AI787387	AI787387 uJ31c10.Y
C 388	17	1.5	435	9	BB778342	BB778342 BB778342	C 461	17	1.5	495	9	AA154649	AA154649 m65b12.r
C 389	17	1.5	436	12	AZ838317	AZ838317 2M0133P22	C 462	17	1.5	496	10	B194052	B194052 B194052
C 390	17	1.5	436	12	AQ040337	AQ040337 HS_5069_B	C 463	17	1.5	496	10	B194993	B194993 B194993
C 391	17	1.5	437	9	BB847450	BB847450 BB847450	C 464	17	1.5	497	12	CNSO1NEP	AI151842 Anopheles
C 392	17	1.5	437	10	BF564211	BF564211 UI-R-C4-A	C 465	17	1.5	498	9	AA013912	AA013912 mB24b04.r
C 393	17	1.5	439	9	AM680793	AM680793 WSI_7_E04	C 466	17	1.5	500	9	AU086883	AU086883 AU086883
C 394	17	1.5	439	9	BB684576	BB684576 BB684576	C 467	17	1.5	500	9	AA565686	AA565686 Ld1_348-D
C 395	17	1.5	441	9	BB845915	BB845915 BB845915	C 468	17	1.5	500	10	BE976379	BE976379 b550a01.Y
C 396	17	1.5	441	10	B1360203	B1360203 387017.MA	C 469	17	1.5	501	10	BE839644	BE839644 RC3-FN015
C 397	17	1.5	443	9	AM563969	AM563969 LG1_275_C	C 470	17	1.5	503	10	B1472831	B1472831 f92ad05.Y
C 398	17	1.5	444	12	AO177112	AO177112 HS_3169.A	C 471	17	1.5	503	10	BM427137	BM427137 pGf2n.PK0
C 399	17	1.5	446	9	AI096270	AI096270 SMACAC24	C 472	17	1.5	504	10	BF391567	BF391567 UI-R-CA1-
C 400	17	1.5	446	10	BF662111	BF662111 mea84c02.	C 473	17	1.5	504	10	BF602358	BF602358 267796.MA
C 401	17	1.5	447	12	AQ853826	AQ853826 nbxb0039E	C 474	17	1.5	506	9	AI956311	AI956311 u173f11.Y
C 402	17	1.5	450	10	BE582699	BE582699 3-1D-MY.P	C 475	17	1.5	506	9	AV672961	AV672961 AV672961
C 403	17	1.5	451	12	AO057114	AO057114 CIT-HSP-2	C 476	17	1.5	507	9	AA987008	AA987008 uc81b10.Y
C 404	17	1.5	451	12	AO307457	AO307457 HS_2236.A	C 477	17	1.5	507	10	BF423450	BF423450 sr95f01.Y
C 405	17	1.5	453	12	AZ239057	AZ239057 RPTC1-23-7	C 478	17	1.5	509	9	AA567106	AA567106 CM01093.5
C 406	17	1.5	454	9	AA693862	AA693862 z154f06.s	C 479	17	1.5	509	10	BF016428	BF016428 uy41b05.Y
C 407	17	1.5	454	10	H98235	H98235 YX09d04.s1	C 480	17	1.5	509	12	AQ498953	AQ498953 HS_5154-B
C 408	17	1.5	455	10	BF654326	BF654326 x512a07.x	C 481	17	1.5	510	9	AA532220	AA532220 UI-R-C4-a
C 409	17	1.5	456	9	AM271943	AM271943 x512a07.x	C 482	17	1.5	513	9	AA918328	AA918328 o142d11.s
C 410	17	1.5	457	9	AV673844	AV673844 AV673844	C 483	17	1.5	513	12	AO328634	AO328634 nbxR0043H
C 411	17	1.5	457	9	BE133829	BE133829 ug11905.x	C 484	17	1.5	515	9	AV397832	AV397832 AV397832
C 412	17	1.5	457	10	BE722839	BE722839 191236.MA	C 485	17	1.5	516	12	AO648437	AO648437 RPTC193-DP
C 413	17	1.5	459	12	BH049443	BH049443 RPTC1-24-2	C 486	17	1.5	517	10	B1244541	B1244541 Eg_PSSL_0
C 414	17	1.5	460	9	AL035961	AL035961 DKRP264E	C 487	17	1.5	519	10	B1244135	B1244135 Eg_CWSL_0
C 415	17	1.5	460	10	B1244524	B1244524 Bg_PSSL_0	C 488	17	1.5	519	10	BM166200	BM166200 EST658723
C 416	17	1.5	460	12	AZ308431	AZ308431 LM0011G21	C 489	17	1.5	520	10	B1244178	B1244178 Eg_CWSL_0
C 417	17	1.5	460	12	AO512667	AO512667 HS_5122.B	C 490	17	1.5	521	10	BG656416	BG656416 jh37b07.x
C 418	17	1.5	462	9	AM721325	AM721325 833013B06	C 491	17	1.5	521	10	W94499	W94499 z613d03.r1
C 419	17	1.5	462	9	AM907652	AM907652 ur96d06.x	C 492	17	1.5	522	9	BB384048	BB384048 BB384048
C 420	17	1.5	462	12	BH283751	BH283751 CH230-49L	C 493	17	1.5	522	12	AQ050393	AQ050393 RPTC1-11-3
C 421	17	1.5	464	9	AM258820	AM258820 um74b02.Y	C 494	17	1.5	523	9	AA848829	AA848829 EST191590
C 422	17	1.5	464	10	AW744632	AW744632 uc13e06.x	C 495	17	1.5	523	10	AM203125	AM203125 f19d412.x
C 423	17	1.5	464	9	BI796941	BI796941 H059E04.E	C 496	17	1.5	523	12	AO282730	AO282730 RPTC11-77
C 424	17	1.5	467	10	AM988801	AM988801 uc11905.Y	C 497	17	1.5	524	9	AM546572	AM546572 L0010B01-
C 425	17	1.5	467	10	BI5771748	BI5771748 R0707033.5	C 498	17	1.5	524	10	BI244373	BI244373 Eg_PSSL_
C 426	17	1.5	468	9	AA250100	AA250100 mx21d08.r	C 499	17	1.5	524	12	B96297	B96297 T23B22TR.T
C 427	17	1.5	468	9	AM822512	AM822512 ug22b08.x	C 500	17	1.5	525	10	BF653070	BF653070 602097960
C 428	17	1.5	470	9	AJ280409	AJ280409 4A3A-AAP-	C 501	17	1.5	526	10	BG561111	BG561111 lb37b07.Y
C 429	17	1.5	472	9	AU086871	AU086871 AU086871	C 502	17	1.5	527	9	AV071548	AV071548 EST503060
C 430	17	1.5	472	12	AZ303162	AZ303162 GSSR-ru210	C 503	17	1.5	529	10	BG603970	BG603970 EST503060
C 431	17	1.5	473	9	AM023468	AM023468 d155c11.Y	C 504	17	1.5	529	10	BI066880	BI066880 pGf1n.PK0
C 432	17	1.5	473	12	AZ588503	AZ588503 LM0396G22	C 505	17	1.5	529	12	AQ181919	AQ181919 HS_3230-A
C 433	17	1.5	474	10	BI371238	BI371238 RE58089.5	C 506	17	1.5	529	12	B52583	B52583 CIT-HSP-200
C 434	17	1.5	475	10	BF545292	BF545292 UI-R-C0-f	C 507	17	1.5	532	9	AV937054	AV937054 AV937054
C 435	17	1.5	476	9	AA432637	AA432637 vd90c03.r	C 508	17	1.5	532	10	BM219149	BM219149 C0920G09-
C 436	17	1.5	477	9	BE027344	BE027344 EFBSTea90	C 509	17	1.5	534	12	AO716330	AO716330 HS_5462-A
C 437	17	1.5	478	10	BF606700	BF606700 273813.MA	C 510	17	1.5	534	12	AZ289131	AZ289131 RPTC1-23-1
C 438	17	1.5	479	9	AA711360	AA711360 vt76a06.r	C 511	17	1.5	535	9	AM568179	AM568179 s157e03.Y
C 439	17	1.5	479	9	AJ393592	AJ393592 AU393592	C 512	17	1.5	536	10	BI240143	BI240143 RE36793.5
C 440	17	1.5	479	10	BG293485	BG293485 602390410	C 513	17	1.5	536	12	AZ892531	AZ892531 RPTC1-24-1
C 441	17	1.5	479	10	BF553118	BF553118 UI-R-C2-n	C 514	17	1.5	537	12	AZ043355	AZ043355 RPTC1-23-3
C 442	17	1.5	480	9	AM982127	AM982127 SSS0047.S	C 515	17	1.5	538	10	BI244103	BI244103 Eg_CWSL_0
C 443	17	1.5	480	10	BM352267	BM352267 1984f04.Y	C 516	17	1.5	539	10	BI244391	BI244391 Eg_CWSL_
C 444	17	1.5	480	10	BF518398	BF518398 SSS0156.S	C 517	17	1.5	540	12	AZ739204	AZ739204 RPTC1-24-1
C 445	17	1.5	481	10	BI591176	BI591176 RH04905.5	C 518	17	1.5	542	10	BG864362	BG864362 602798242
C 446	17	1.5	481	10	BE585926	BE585926 Est4pT7	C 519	17	1.5	543	10	BI983593	BI983593 f185e10.x
C 447	17	1.5	481	12	AZ170649	AZ170649 SP_0117.A	C 520	17	1.5	543	12	AO577215	AO577215 nbxR0090J
C 448	17	1.5	483	12	BH105982	BH105982 RPTC1-24-3	C 521	17	1.5	544	9	AI387230	AI387230 GH17692.5
C 449	17	1.5	484	9	AM318956	AM318956 uni10a03.Y	C 522	17	1.5	545	9	AM055772	AM055772 SMACAC38
C 450	17	1.5	484	12	AZ288012	AZ288012 RPTC1-23-1	C 523	17	1.5	545	10	BF223660	BF223660 7q78e06.x
C 451	17	1.5	485	9	AI987595	AI987595 u186b11.Y	C 524	17	1.5	546	10	BM243763	BM243763 KO701E02-
C 452	17	1.5	485	10	BI033926	BI033926 QV2-NN200	C 525	17	1.5	546	12	AO537931	AO537931 RPTC1-11-3
C 453	17	1.5	485	10	N31106	N31106 YX52b01.r1	C 526	17	1.5	547	9	AO447635	AO447635 mgxR0008M
C 454	17	1.5	487	10	BR960083	BR960083 QV2-NN004	C 527	17	1.5	548	9	AI135744	AI135744 GH13606.5
C 455	17	1.5	487	10	BG710769	BG710769 pG11n.PK0	C 528	17	1.5	548	10	BI593456	BI593456 RH1514.5

C 675	17	1.5	679	10	BE532770	BE532770 601233916	C 748	17	1.5	762	9	AV404062	AV404062
C 676	17	1.5	679	12	AO566429	AO566429 HS-2096.A	C 749	17	1.5	763	10	BI58679	BI58679
C 677	17	1.5	681	10	BI193392	BI193392 602947024	C 750	17	1.5	764	9	AI1317374	AI1317374
C 678	17	1.5	682	12	A2524027	A2524027 226PBC10	C 751	17	1.5	767	12	BH399000	BH399000
C 679	17	1.5	683	10	AW913495	AW913495 uF53f05.Y	C 752	17	1.5	768	10	BG972346	BG972346
C 680	17	1.5	683	10	BI102350	BI102350 602885691	C 753	17	1.5	769	9	AU003365	AU003365
C 681	17	1.5	684	10	AW319624	AW319624 um99f06.x	C 754	17	1.5	769	12	BH510892	BH510892
C 682	17	1.5	685	9	AI514098	AI514098 uJ12b10.x	C 755	17	1.5	772	12	AO739758	AO739758
C 683	17	1.5	686	9	AI513977	AI513977 GH27011.5	C 756	17	1.5	780	9	AA968100	AA968100
C 684	17	1.5	688	9	AU004500	AU004500 AU004500	C 757	17	1.5	780	9	BG422548	BG422548
C 685	17	1.5	690	10	AM261689	AM261689 um90h01.x	C 758	17	1.5	781	9	AU122743	AU122743
C 686	17	1.5	690	10	BI213754	BI213754 RE19247.5	C 759	17	1.5	781	10	BI102803	BI102803
C 687	17	1.5	692	9	BE148614	BE148614 MR0-HR024	C 760	17	1.5	782	10	BF687125	BF687125
C 688	17	1.5	692	12	A2184785	A2184785 SP-1003.B	C 761	17	1.5	783	12	AO857998	AO857998
C 689	17	1.5	693	9	AI267069	AI267069 uJ10d08.x	C 762	17	1.5	784	9	AI115991	AI115991
C 690	17	1.5	694	9	AU138198	AU138198 AU138198	C 763	17	1.5	784	12	AO876204	AO876204
C 691	17	1.5	696	9	AM260285	AM260285 um76a11.x	C 764	17	1.5	788	12	BH559362	BH559362
C 692	17	1.5	698	9	AW319673	AW319673 um01h10.x	C 765	17	1.5	790	9	AU079836	AU079836
C 693	17	1.5	698	12	AQ256136	AQ256136 nbxb0011D	C 766	17	1.5	790	10	BI143892	BI143892
C 694	17	1.5	699	9	AI649039	AI649039 UK34e04.x	C 767	17	1.5	791	12	AO687266	AO687266
C 695	17	1.5	699	12	AO075055	AO075055 CIT-HSP-2	C 768	17	1.5	791	12	AZ202357	AZ202357
C 696	17	1.5	699	12	BH456484	BH456484 BOHRT544F	C 769	17	1.5	791	12	BH446260	BH446260
C 697	17	1.5	702	9	AI267142	AI267142 uJ11d08.x	C 770	17	1.5	791	12	AO292006	AO292006
C 698	17	1.5	702	9	AU004414	AU004414 AU004414	C 771	17	1.5	791	12	CNS00080	CNS00080
C 699	17	1.5	704	12	AQ529553	AQ529553 RPCI-11-3	C 772	17	1.5	795	12	CNS0320L	CNS0320L
C 700	17	1.5	705	12	AL654122	AL654122 AL654122	C 773	17	1.5	796	9	AI647777	AI647777
C 701	17	1.5	705	12	BH183124	BH183124 022.L-18-	C 774	17	1.5	796	9	BF787922	BF787922
C 702	17	1.5	708	12	CNS070D5	AL650075.T3 end of	C 775	17	1.5	797	12	BG707213	BG707213
C 703	17	1.5	708	9	AI132447	AI132447 ue25c10.x	C 776	17	1.5	800	9	AI119083	AI119083
C 704	17	1.5	708	9	AL556141	AL556141 AL556141	C 777	17	1.5	800	9	AU079850	AU079850
C 705	17	1.5	709	9	AI118358	AI118358 ue23c04.x	C 778	17	1.5	803	12	AO575528	AO575528
C 706	17	1.5	711	9	AI649353	AI649353 UK30905.x	C 779	17	1.5	808	10	BI664288	BI664288
C 707	17	1.5	715	9	AI405844	AI405844 GH25985.5	C 780	17	1.5	809	12	AO257607	AO257607
C 708	17	1.5	716	9	BJ0088409	BJ0088409 BJ0088409	C 781	17	1.5	810	10	BI117268	BI117268
C 709	17	1.5	717	10	BG471712	BG471712 602513436	C 782	17	1.5	810	10	BI664647	BI664647
C 710	17	1.5	718	12	A2660690	A2660690 1M0538372	C 783	17	1.5	810	12	CNS00920	CNS00920
C 711	17	1.5	720	9	AU136782	AU136782 AU136782	C 784	17	1.5	811	9	AW107500	AW107500
C 712	17	1.5	720	10	BE314237	BE314237 601153044	C 785	17	1.5	811	12	BH382329	BH382329
C 713	17	1.5	720	10	BF320332	BF320332 u252e04.Y	C 786	17	1.5	815	9	AA968324	AA968324
C 714	17	1.5	721	9	AI316510	AI316510 uJ14f02.x	C 787	17	1.5	816	9	AW106903	AW106903
C 715	17	1.5	721	9	AI597338	AI597338 mJ90a08.Y	C 788	17	1.5	817	12	BH095860	BH095860
C 716	17	1.5	721	12	AO576521	AO576521 nbxb0089E	C 789	17	1.5	820	9	AI788951	AI788951
C 717	17	1.5	722	9	AI132433	AI132433 ue25b07.x	C 790	17	1.5	820	10	BF788778	BF788778
C 718	17	1.5	722	10	BE788991	BE788991 602104835	C 791	17	1.5	821	10	BI218037	BI218037
C 719	17	1.5	723	12	AO687207	AO687207 nbxb0073P	C 792	17	1.5	823	12	AO686566	AO686566
C 720	17	1.5	723	12	BH395453	BH395453 AG-ND-147	C 793	17	1.5	823	12	BH568797	BH568797
C 721	17	1.5	724	10	BE914814	BE914814 601667838	C 794	17	1.5	824	10	BI854319	BI854319
C 722	17	1.5	724	12	BH300162	BH300162 CH230-109	C 795	17	1.5	826	9	AI790678	AI790678
C 723	17	1.5	725	9	AI314702	AI314702 uJ27g01.x	C 796	17	1.5	828	10	BG567790	BG567790
C 724	17	1.5	725	10	BG718515	BG718515 602666573	C 797	17	1.5	829	9	AI649179	AI649179
C 725	17	1.5	725	10	BI103054	BI103054 602888689	C 798	17	1.5	833	9	AI647699	AI647699
C 726	17	1.5	725	12	A2985759	A2985759 2M0267P12	C 799	17	1.5	833	10	BI554921	BI554921
C 727	17	1.5	726	12	AE131936	AZ3131936 CSUNDB011	C 800	17	1.5	836	10	BE268283	BE268283
C 728	17	1.5	726	12	AE613041	AZ613041 1M0441P12	C 801	17	1.5	843	9	AI648972	AI648972
C 729	17	1.5	727	10	BE284099	BE284099 601099296	C 802	17	1.5	845	12	AE532784	AE532784
C 730	17	1.5	727	10	BE306118	BE306118 601100414	C 803	17	1.5	846	12	BH562524	BH562524
C 731	17	1.5	728	12	AO289732	AO289732 nbxb00035H	C 804	17	1.5	848	9	AW106932	AW106932
C 732	17	1.5	734	10	BE584963	BE584963 6020908849	C 805	17	1.5	851	10	BG495516	BG495516
C 733	17	1.5	735	10	BI412195	BI412195 602989986	C 806	17	1.5	854	12	AO687775	AO687775
C 734	17	1.5	737	12	AG097007	AG097007 Pan.Trog1	C 807	17	1.5	857	9	AI746298	AI746298
C 735	17	1.5	738	9	AV700539	AV700539 AV700539	C 808	17	1.5	857	10	BF786310	BF786310
C 736	17	1.5	743	10	BG809267	BG809267 mgh60018x	C 809	17	1.5	857	12	BH092908	BH092908
C 737	17	1.5	743	10	BG969294	BG969294 602836765	C 810	17	1.5	861	9	AI113964	AI113964
C 738	17	1.5	746	12	AZ879307	AZ879307 RPT-23-1	C 811	17	1.5	861	9	AI987711	AI987711
C 739	17	1.5	747	12	BH581640	BH581640 BOHLEF30TF	C 812	17	1.5	862	10	BI663569	BI663569
C 740	17	1.5	747	12	CNS00BE7	AI056863 Drosoph11	C 813	17	1.5	862	10	BI948892	BI948892
C 741	17	1.5	750	12	AO349409	AO349409 RPT11-11	C 814	17	1.5	864	12	BI260075	BI260075
C 742	17	1.5	751	9	AU167238	AU167238 6029004512	C 815	17	1.5	864	12	CNS00913	CNS00913
C 743	17	1.5	753	12	BI154720	BI154720 6029004512	C 816	17	1.5	867	10	BE874924	BE874924
C 744	17	1.5	754	12	AO578259	AO578259 nbxb0092F	C 817	17	1.5	868	10	BG300655	BG300655
C 745	17	1.5	756	12	AO326081	AO326081 nbxb00024L	C 818	17	1.5	869	10	BI143894	BI143894
C 746	17	1.5	757	10	BG765608	BG765608 602738502	C 819	17	1.5	870	9	AL537110	AL537110
C 747	17	1.5	760	9	AW475206	AW475206 um72h10.Y	C 820	17	1.5	871	10	BI869842	BI869842

821	17	1.5	875	9	AA203353	AA203353	zx57b09..r	C 894	17	1.5	1101	12	CNS002V9	AL063511	Drosophila
C 822	17	1.5	876	10	BI412109	BI412109	602964860	C 895	17	1.5	1101	12	CNS00CSN	AL059368	Drosophila
C 823	17	1.5	876	10	BI646433	BI646433	603279010	C 896	17	1.5	1101	12	CNS00HVZ	AL070413	Drosophila
C 824	17	1.5	879	12	CNS05NKS	AL345493	Tetradon	C 897	17	1.5	1101	12	CNS05471	AL030547	Tetradon
C 825	17	1.5	881	10	BI147088	BI147088	602913360	C 898	17	1.5	1102	10	BM460639	BM460639	Agencourt
C 826	17	1.5	884	10	BG295757	BG295757	602393210	C 899	17	1.5	1147	10	BG024236	BG024236	602302954
C 827	17	1.5	884	10	BE570618	BE570618	601329223	C 900	17	1.5	1156	10	BE729821	BE729821	601564735
C 828	17	1.5	886	10	BE784356	BE784356	602110131	C 901	17	1.5	1160	12	CNS007J9	AL067337	Drosophila
C 829	17	1.5	891	10	BE728760	BE728760	601564447	C 902	17	1.5	1201	12	CNS0010X	AL060097	Drosophila
C 830	17	1.5	892	10	BE792416	BE792416	601585162	C 903	17	1.5	1227	10	BE260063	BE260063	601150949
C 831	17	1.5	892	12	AZ681927	AZ681927	ENTVI1TR	C 904	17	1.5	1321	10	BE166709	BE166709	601776224
C 832	17	1.5	892	12	BI157767	BI157767	ENTR82TR	C 905	17	1.5	1339	10	BE294378	BE294378	004PBE01
C 833	17	1.5	893	10	BI410036	BI410036	602962519	C 906	17	1.5	1522	10	BE694004	BE694004	602082592
C 834	17	1.5	897	12	CNS03DM7	AL261304	Tetradon	C 907	17	1.5	1565	11	AK015326	AK015326	Mus muscu
C 835	17	1.5	898	10	BF315074	BF315074	601902510	C 908	17	1.5	1602	10	BG165628	BG165628	602345114
C 836	17	1.5	898	12	AZ691137	AZ691137	ENTM68TR	C 909	17	1.5	1813	10	BE237826	BE237826	601842371
C 837	17	1.5	899	12	BI133763	BI133763	ENTM682TR	C 910	17	1.5	2054	11	BC022902	BC022902	Mus muscu
C 838	17	1.5	900	9	AL666200	AL666200	AL666200	C 911	17	1.5	3065	11	AK019548	AK019548	Mus muscu
C 839	17	1.5	900	12	BI177432	BI177432	009_D_10-	C 912	17	1.4	50	10	BG223087	BG223087	nah13604
C 840	17	1.5	900	12	CNS07J38	AL614390	T7 end of	C 913	16	1.4	55	10	BE542738	BE542738	601066341
C 841	17	1.5	901	12	AZ535919	AZ535919	ENTB096TR	C 914	16	1.4	61	9	AA546711	AA546711	VK55C02..r
C 842	17	1.5	901	12	BI159707	BI159707	ENTTC3TR	C 915	16	1.4	87	12	AZ780134	AZ780134	2M0017108
C 843	17	1.5	903	10	BF785598	BF785598	602112386	C 916	16	1.4	104	9	AU209499	AU209499	AU209499
C 844	17	1.5	904	12	BI167215	BI167215	ENTSO18TR	C 917	16	1.4	106	10	BG893358	BG893358	dae19f02.
C 845	17	1.5	911	10	BF780753	BF780753	602103027	C 918	16	1.4	111	9	AA591875	AA591875	V147H04..r
C 846	17	1.5	914	10	BF780409	BF780409	602103928	C 919	16	1.4	126	9	AM881548	AM881548	RC4-OT003
C 847	17	1.5	915	10	BG497847	BG497847	602543137	C 920	16	1.4	127	12	AZ310281	AZ310281	1M0025K12
C 848	17	1.5	920	12	CNS03MA1	AL250498	Tetradon	C 921	16	1.4	129	9	BE167709	BE167709	CM3-HT051
C 849	17	1.5	923	10	BI102605	BI102605	602888128	C 922	16	1.4	131	10	BI435853	BI435853	EST538614
C 850	17	1.5	923	12	CNS06UJ7	AL415277	T7 end of	C 923	16	1.4	136	10	BE937719	BE937719	PM2-TN002
C 851	17	1.5	927	12	AQ688304	AQ688304	nxh0077K	C 924	16	1.4	137	9	AI508628	AI508628	vb55g11..y
C 852	17	1.5	928	10	BF787496	BF787496	602113914	C 925	16	1.4	143	9	AA386760	AA386760	vd53g11..r
C 853	17	1.5	928	10	BF787496	BF787496	602113914	C 926	16	1.4	143	12	AZ239310	AZ239310	RCPT-23-7
C 854	17	1.5	928	10	BF787496	BF787496	602113914	C 927	16	1.4	142	10	T80393	T80393	y05d12..r1
C 855	17	1.5	929	12	CNS00CDN	AL056744	Drosophila	C 928	16	1.4	146	10	BI002006	BI002006	MR2-HN006
C 856	17	1.5	931	10	BI192727	BI192727	602349145	C 929	16	1.4	147	9	AA069049	AA069049	zm11h02..r
C 857	17	1.5	931	10	BF344941	BF344941	602014259	C 930	16	1.4	148	9	AA880702	AA880702	vx30d02..r
C 858	17	1.5	933	12	CNS0310C	AL245901	Tetradon	C 931	16	1.4	149	9	BE072686	BE072686	RC2-BT054
C 859	17	1.5	934	10	BG473633	BG473633	602515986	C 932	16	1.4	152	10	BF063806	BF063806	7h96d08..x
C 860	17	1.5	934	10	BF311362	BF311362	601896765	C 933	16	1.4	153	10	T81194	T81194	y096c08..r1
C 861	17	1.5	935	12	AZ672871	AZ672871	ENTFAS7TR	C 934	16	1.4	162	12	AO658652	AO658652	Sheared D
C 862	17	1.5	935	12	BI138870	BI138870	ENTM037TR	C 935	16	1.4	163	9	BE072850	BE072850	RC2-BT054
C 863	17	1.5	938	10	BM396759	BM396759	5009-0-24	C 936	16	1.4	165	9	AM368869	AM368869	IL5-HT019
C 864	17	1.5	940	12	CNS02M62	AL203699	Tetradon	C 937	16	1.4	169	9	AV035412	AV035412	AV035412
C 865	17	1.5	944	10	BF159933	BF159933	601768105	C 938	16	1.4	171	9	AI555058	AI555058	UI-R-C2P-
C 866	17	1.5	947	10	BG259538	BG259538	602378657	C 939	16	1.4	175	9	AM454193	AM454193	zebl1070
C 867	17	1.5	948	9	AI513805	AI513805	GH26904..5	C 940	16	1.4	179	9	BB200792	BB200792	
C 868	17	1.5	953	12	BI155124	BI155124	ENTSR11TR	C 941	16	1.4	181	9	BE072681	BE072681	RC2-BT054
C 869	17	1.5	959	12	CNS05HRQ	AL337895	Tetradon	C 942	16	1.4	186	10	BI127896	BI127896	G067P62Y
C 870	17	1.5	960	9	AL666445	AL666445	AL666445	C 943	16	1.4	188	9	AA420191	AA420191	vF51f08..r
C 871	17	1.5	964	12	CNS05AYD	AL329134	Tetradon	C 944	16	1.4	188	10	BI169905	BI169905	REI11212.5
C 872	17	1.5	965	10	BM008624	BM008624	603618274	C 945	16	1.4	188	12	BI341484	BI341484	CH230-111
C 873	17	1.5	970	12	CNS02X0J	AL217756	Tetradon	C 946	16	1.4	191	12	BE156433	BE156433	OVO-HT036
C 874	17	1.5	972	12	CNS07AMS	AL436778	T7 end of	C 947	16	1.4	191	10	BF639351	BF639351	NEP011061
C 875	17	1.5	973	10	BI739342	BI739342	603359652	C 948	16	1.4	199	12	AO635215	AO635215	SBR4 AGS-
C 876	17	1.5	973	12	CNS03VAV	AL262195	Tetradon	C 949	16	1.4	202	9	AM3332410	AM3332410	AV143483
C 877	17	1.5	974	12	CNS005MF	AL059370	Drosophila	C 950	16	1.4	203	9	AV143483	AV143483	AV359607
C 878	17	1.5	985	12	CNS005M4	AL059370	Drosophila	C 951	16	1.4	206	9	AV359607	AV359607	AV359607
C 879	17	1.5	997	10	BF687782	BF687782	602066832	C 952	16	1.4	207	9	BE162771	BE162771	OV3-HT045
C 880	17	1.5	1001	10	BI414294	BI414294	602996585	C 953	16	1.4	208	9	AM314065	AM314065	9842 MARC
C 881	17	1.5	1002	10	BG755130	BG755130	602771146	C 954	16	1.4	211	12	BH033619	BH033619	RCPT-24-3
C 882	17	1.5	1007	10	BG297012	BG297012	602394862	C 955	16	1.4	213	12	AZ752441	AZ752441	RCPT-24-1
C 883	17	1.5	1021	12	CNS006JY	AL259374	Tetradon	C 956	16	1.4	214	10	BF761364	BF761364	RC2-CS001
C 884	17	1.5	1024	12	CNS0374L	AL259374	Tetradon	C 957	16	1.4	216	9	BI147886	BI147886	daa38e02..
C 885	17	1.5	1030	12	CNS07BGO	AL437854	T7 end of	C 958	16	1.4	216	10	BG346537	BG346537	daa38e02..
C 886	17	1.5	1031	12	BI2303	BI2303	F16B11-T7 I	C 959	16	1.4	217	10	BG156300	BG156300	sa873h10.
C 887	17	1.5	1035	12	CNS04ODT	AL288777	Tetradon	C 960	16	1.4	220	10	BF611275	BF611275	dg77h12..y
C 888	17	1.5	1046	10	BF785777	BF785777	602112294	C 961	16	1.4	220	9	AI950291	AI950291	wq38h05..x
C 889	17	1.5	1049	12	CNS04MPZ	AL297142	Tetradon	C 962	16	1.4	221	9	BE049807	BE049807	NXNY_144
C 890	17	1.5	1085	12	CNS00ZXP	AL082829	Drosophila	C 963	16	1.4	222	9	AM649477	AM649477	EST327931
C 891	17	1.5	1090	12	CNS05BEF	AL330433	Tetradon	C 964	16	1.4	223	10	BM278729	BM278729	As. ltrg. 66
C 892	17	1.5	1101	12	CNS000MZ	AL0633247	Drosophila	C 965	16	1.4	223	10	H30565	H30565	yp45f03..s1
C 893	17	1.5	1101	12	CNS001T6	AL061332	Drosophila	C 966	16	1.4	227	9	AV885030	AV885030	

C 967	16	1.4	227	10	BG346546	BG346546 daa3pa12.
C 968	16	1.4	229	9	BB057250	BB057250 BB057250
C 969	16	1.4	230	10	BF199025	BF199025 249060 MA
C 970	16	1.4	232	9	BB186527	BB186527 BB186527
C 971	16	1.4	233	10	BJ004458	BJ004458 BJ004458
C 972	16	1.4	233	10	H39193	H39193 yn84d1.r1
C 973	16	1.4	233	10	T39491	T39491 ya06f01.r1
C 974	16	1.4	235	9	AV356606	AV356606 AV356606
C 975	16	1.4	235	10	T75805	T75805 10583 Lambda
C 976	16	1.4	236	9	AV217051	AV217051 AV217051
C 977	16	1.4	236	10	BI887991	BI887991 ZF637-1-0
C 978	16	1.4	237	9	AA078111	AA078111 7h14C03 C
C 979	16	1.4	237	10	F05928	F05928 HSC0P0601 n
C 980	16	1.4	238	9	A1764895	A1764895 MEG0750
C 981	16	1.4	238	9	A1772835	A1772835 EST253935
C 982	16	1.4	238	9	AV336510	AV336510 AV336510
C 983	16	1.4	238	9	AV561972	AV561972 AV561972
C 984	16	1.4	238	10	BG124622	BG124622 EST470184
C 985	16	1.4	240	9	AU073887	AU073887 AU073887
C 986	16	1.4	240	10	BM434261	BM434261 1RT06C12
C 987	16	1.4	241	9	AM843435	AM843435 CM0-CM003
C 988	16	1.4	241	9	BB198000	BB198000 BB198000
C 989	16	1.4	241	10	BE583001	BE583001 3-4H-MY P
C 990	16	1.4	241	12	AZ009581	AZ009581 RPTC-23-P-3
C 991	16	1.4	241	12	AO193779	AO193779 CIT-HSP-2
C 992	16	1.4	242	9	BB808166	BB808166 BB808166
C 993	16	1.4	242	10	BG630074	BG630074 CC-estfLCL
C 994	16	1.4	243	9	AV229167	AV229167 AV229167
C 995	16	1.4	243	12	AZ645100	AZ645100 IM0510B19
C 996	16	1.4	247	10	BI730868	BI730868 603551891
C 997	16	1.4	249	9	AV275280	AV275280 AV275280
C 998	16	1.4	249	9	AV315445	AV315445 AV315445
C 999	16	1.4	252	9	AV230398	AV230398 AV230398
C 1000	16	1.4	252	10	BG631665	BG631665 CC-estfLCL

ALIGNMENTS

RESULT	1
A1176234/c	
LOCUS	A1176234
DEFINITION	EST219815 Normalized rat ovary, Bento Soares Rattus sp. cDNA clone
ACCESSION	ROXB092.3 end, mRNA sequence.
VERSION	A1176234
KEYWORDS	A1176234.1 GI:3726872
SOURCE	EST.
ORGANISM	Rattus sp.
	Rattus sp.
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
	Rattus.
REFERENCE	1 (bases 1 to 348)
AUTHORS	Lee,N.H., Glodok,A., Chandra,I., Mason,T.M., Quackenbush,J., Kerlavage,A.R. and Adams,M.D.
TITLE	Rat Genome Project: Generation of a Rat EST (RESTR) Catalog & Rat Gene Index
JOURNAL	Unpublished (1998)
COMMENT	Other ESTs: TC48377
	Contact: Lee, NH
	The Institute for Genomic Research
	9712, Medical Center Drive, Rockville, MD 20850, USA
	Tel: (301)-838-3529
	Fax: (301)-838-0208
	Email: nhlee@tigr.org
FEATURES	Seq primer: M13-21.
source	Location/Qualifiers
	I..348

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FEATURES
source
location/Qualifiers
1..348
/organism="Rattus sp."
/db_xref="ATCC (inhost):2031231"
/db_xref="taxon:10118"
/clone="ROV092"
/clone_1id="Normalized rat ovary, Bento Soares"

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/note="Organ: ovary; Vector: pf7f3Pac; Site_1: Ecore1;
Site_2: NotI"
BASE COUNT      79 a      85 c      104 g      80 t
ORIGIN
Query Match      1.9%; Score 22; DB 9; Length 348;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 935 tcatggagctcacacctgatatt 956
|||||
Db 331 TCATGGGCTTCACCTGATGTT 310

```

[illegible]

```

FEATURES
source
    Contact: Lee, NH
    The Institute for Genomic Research
    9712, Medical Center Drive, Rockville, MD 20850, USA
    Tel: (301)-838-3529
    Fax: (301)-838-0208
    Email: nhlee@tigr.org
    Seq primer: M13-21.
    Location/Qualifiers
        1..354
        /organism="Rattus sp."
        /db_xref="ATCC (lnhost):2034870"
        /db_xref="taxon:10118"
        /clone="RSPB078"
        /clone_1bp="Normalized rat spleen, Bento Soares"
        /note="Organ: Spleen; Vector: pT713pac; Site_1: EcoRI;
        Site_2: NotI"
BASE COUNT
85 a      80 c      112 g      77 t
ORIGIN

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Query Match	1.9%	Score 22	DB 9	Length 354
Best Local Similarity	100.0%	Pred. No. 2		
Matches 22	Conservative 0	Mismatches 0	Indels 0	Gaps 0
OY	935	tcatgggccttcacctgatgtt	956	
Db	310	TCATGGGCTTCACCCCTGATGTT	289	
RESULT	3			
LOCUS	A0187817	585 bp	DNA	linear
DEFINITION	HS 3141 B1 D09 MR CIT	Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate-3141 COL-17 Row-H		GSS 03-NOV-1998
ACCESSION	A0187817			
VERSION	A0187817.1	GI:3587229		
KEYWORDS	GSS.			
SOURCE	human.			

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 585)
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.
TITLE Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
JOURNAL Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
MEDLINE 99380589
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: <http://www.htsc.washington.edu>

FEATURES
SOURCE
Location/Qualifiers
1..585
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/sex="male"
/note="Organ: sperm; Vector: pBelBAC11; BAC Clones in
E-Coli DH10B"
BASE COUNT 149 a 135 c 108 g 187 t 6 others
ORIGIN

Query Match 1.8%; Score 21; DB 12; Length 585;
Best Local Similarity 100.0%; Pred. No. 7.2;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 46 tgcgtcctgcgtctactat 66
|||||
Db 93 TGCTGCTGCTGCTACTTAT 113

RESULT 4
LOCUS A0891144 627 bp DNA linear GSS 10-NOV-1999
DEFINITION HS-3142_AL-A06_MR CIT Approved Human Genomic Sperm Library D Homo
sapiens genomic clone Plate-3142 Col-11 Row-A, DNA sequence.
ACCESSION A0891144
VERSION A0891144.1 GI:6347334
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 627)
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.
TITLE Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
JOURNAL Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
MEDLINE 99380589
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: <http://www.htsc.washington.edu>

Plate: 3142 row: A column: 11
Seq primer: M13 Reverse
Class: BAC ends
High quality sequence stop: 627.
Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/sex="male"
/note="Organ: sperm; Vector: pBelBAC11; BAC Clones in
E-Coli DH10B"
BASE COUNT 154 a 129 c 105 g 221 t 18 others
ORIGIN

Query Match 1.8%; Score 21; DB 12; Length 627;
Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 46 tgcgtcctgcgtctactat 66
|||||
Db 120 TGCTGCTGCTGCTACTTAT 140

RESULT 5
LOCUS BB515310/C 282 bp mRNA linear EST 28-JUL-2000
DEFINITION BB515310 RIKEN full-length enriched, 16 days neonate heart Mus
musculus cDNA clone D830007M21 3' similar to NM_008509 Mus musculus
lipoprotein lipase (Lpl), mRNA sequence.
ACCESSION BB515310
VERSION BB515310.1 GI:9566768
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 282)
AUTHORS Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T., Carninci,
P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N.,
Hirozane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M.,
Iizawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N.,
Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C., Kusakabe,M.,
Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y.,
Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K., Shibata,K., Shibata,
Y., Shigemoto,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Sugahara,Y.,
Suzuki,H., Suzuki,H., Tagawa,A., Takahashi,F., Tomihaga,N., Toya,
T., Tsunoda,Y., Watabiki,A., Watanabe,S., Yamamura,T., Yamanaka,I.,
Yano,R., Yasunishi,A., Yokota,T., Yoshida,K., Yoshiki,A., Yoshino,
M., Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Konno,H., et al.)
TITLE Unpublished (2000)
JOURNAL Contact: Yoshihide Hayashizaki
LABORATORY Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL:<http://genome.gsc.riken.go.jp/>
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,
N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermolabile enzymes by
trehalose and its application for the synthesis of full length
cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Katsunai,T., Akiyama,J., Shibata,K., Iizawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,
Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation
system. Genome Res. 9 (5), 463-470 (1999)


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/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone.lib="NIH-BMAP-MBG_N"
/dev_stage="27-32 days"
/lab_host="DH10B (Life Technologies)"
/notes="vector: pRT3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The
NIH-BMAP-MBG_N library is a normalized library constructed
from mouse basal ganglia. The tag is a string of 5
nucleotides present between the Not I site and the
oligo-dT track. The library was constructed as described
by Bonaldi, Lennon and Soares, Genome Research 6: 791-806
, 1996. Tissue provided by Ms. Annie Novakovich,
Zivic-Miller Laboratories.
TAG_LIB=NIH-BMAP-MBG_N
TAG_TISSUE=basal ganglia
TAG_SEQ=GTAC"

BASE COUNT      89 a      84 c      99 g      98 t
ORIGIN

Query Match      1.8%; Score 20; DB 9; Length 370;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 938 tgggttcacccctgatgttc 957
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Db 366 TGGGCTTCACCCCTGATGTTTC 347

RESULT 8
AA590068      373 bp      mRNA      linear      EST 16-SEP-1997
LOCUS      vnt7e06.r1 Barstead mouse proximal colon MRLRB6 Mus musculus cDNA
DEFINITION      clone IMAGE:1025314 5', mRNA sequence.
ACCESSION      AA590068
VERSION      AA590068.1 GI:2403448
KEYWORDS      EST.
SOURCE      house mouse.
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 373)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisels,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
The WashU-HHMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:576090
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 366.

FEATURES
source
1. 373
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone.lib="IMAGE:1025314"
/clone.lib="Barstead mouse proximal colon MRLRB6"
/dev_stage="7 day juvenile"
/lab_host="DH10B"

/note="vector: pRT3D-Pac (Pharmacia) with a modified
polylinker; Site_1: EcoRI; Site_2: NotI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5'
TGTTCAGATCTGAGTGGAGCGGCGCCCTTTTCTTTTCTTTTCTTTTCTTTT
3']. double-stranded cDNA was ligated to Eco RI adaptors
[ATTCGGATCTTC], digested with Not I and Eco RI sites of the
Not I and Eco RI sites of the modified pRT3D vector.
Library constructed by Bob Barstead."

BASE COUNT      87 a      104 c      87 g      95 t
ORIGIN

Query Match      1.8%; Score 20; DB 9; Length 373;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 938 tgggttcacccctgatgttc 957
|||||
Db 25 TGGGCTTCACCCCTGATGTTTC 44

RESULT 9
W30259      376 bp      mRNA      linear      EST 11-SEP-1996
LOCUS      mc25a06.r1 Soares mouse p3NMF19.5 Mus musculus cDNA clone
DEFINITION      IMAGE:349522 5', mRNA sequence.
ACCESSION      W30259
VERSION      W30259.1 GI:1310407
KEYWORDS      EST.
SOURCE      house mouse.
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 376)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisels,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
The WashU-HHMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:221322
Seq primer: EMP1mer
High quality sequence stop: 372.

FEATURES
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1. 376
/organism="Mus musculus"
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/dev_stage="19.5 dpc total fetus"
/lab_host="DH10B (ampicillin resistant)"
/notes="vector: pRT3D (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5'
TGTTCAGATCTGAGTGGAGCGGCGCCCTTTTCTTTTCTTTTCTTTTCTTTT
3']. double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and Eco RI sites of
the Not I and Eco RI sites of a modified pRT3D vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento
Soares and M.Fatima Bonaldi. RNA was kindly provided by
Dr. Minoru Ko (Wayne State University)."
```

BASE COUNT

60 a 116 c 103 g 97 t

Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:427434

Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 387.

FEATURES

source

1. .409

Location/Qualifiers

/organism="Mus musculus"

/db_xref="taxon:10090"

/clone="IMAGE:693874"

/clone_lib="Soares mouse NML"

/tissue_type="Liver"

/lab_host="DHI0B"

/note="Vector: pT7T3D-Pac (Pharmacia) with a modified

polylinker. Site_1: Not I; Site_2: Eco RI; 1st strand cDNA

was primed with a Not I - oligo(dt) primer [5,

TGTTACCAATCTGAAGTGGAGCGCGCGCAATCTTTTTTTTTTTT 3'];

double-stranded cDNA was ligated to Eco RI adaptors

(Pharmacia), digested with Not I and cloned into the Not I

and Eco RI sites of the modified pT7T3 vector. Library

constructed and normalized by Bento Soares and M.Fatima

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/note="Organ: kidney; Vector: pCMV-SPORE6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library. I"

BASE COUNT 116 a 110 c 87 g 100 t

Query Match 1.8%; Score 20; DB 10; Length 413;

Best Local Similarity 100.0%; Pred. No. 24;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 938 tgggctcaccctgattgc 957

|||||

Db 50 TGGGCTTACCCCTGATGTTTC 69

RESULT 14

AA245797

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CONTACT

UNPUBLISHED

WASHU-HHMI

WASHINGTON

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:419127

Seq primer: -28m13 rev2 ET from Amersham

High quality sequence stop: 425.

Location/Qualifiers

1. .426

/organism="Mus musculus"

/db_xref="taxon:10090"

/clone="IMAGE:679423"

/clone_lib="Soares mouse NML"

/tissue_type="Liver"

/lab_host="DHI0B"

/note="Vector: pT7T3D-Pac (Pharmacia) with a modified

polylinker. Site_1: Not I; Site_2: Eco RI; 1st strand cDNA

was primed with a Not I - oligo(dt) primer [5,

TGTTACCAATCTGAAGTGGAGCGCGCGCAATCTTTTTTTTTTTT 3'];

double-stranded cDNA was ligated to Eco RI adaptors

(Pharmacia), digested with Not I and cloned into the Not I

and Eco RI sites of the modified pT7T3 vector. Library

constructed and normalized by Bento Soares and M.Fatima

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BASE COUNT 77 a 137 c 100 g 104 t 8 others

ORIGIN

Query Match

Best Local Similarity

Matches

20; Conservative

0; Mismatches

0; Indels

0; Gaps

0;

1.8%; Score 20; DB 9; Length 426;

Pred. No. 24;

0; Indels

0; Gaps

0;

0;

0;

0;

0;

0;

Oy 938 tgggctcaccctgatgttc 957
 |||||||
 Db 202 TGGGCTTCACCCCTGATGTTC 221

Search completed: May 7, 2002, 17:25:00
 Job time: 8130 sec

RESULT 15
 AI042890 428 bp mRNA linear EST 01-JUL-1998
 LOCUS uc77c05.x1 Sugano mouse liver mla Mus musculus cDNA clone
 DEFINITION IMAGE:1431656 3', mRNA sequence.
 ACCESSION AI042890
 VERSION AI042890.1 GI:3286150
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 REFERENCE 1 (bases 1 to 428)
 Mairra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
 Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
 Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
 Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
 Waterston,R.
 TITLE The WashU-HMI Mouse EST Project
 JOURNAL Unpublished (1996)
 COMMENT Contact: Mairra M/Mouse EST Project
 WashU-HMI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@watson.wustl.edu
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:915724
 Seq primer: custom primer used
 High quality sequence stop: 351.
 Location/Qualifiers
 1. 428
 /organism="Mus musculus"
 /strain="C57BL"
 /db_xref="taxon:10090"
 /clone="IMAGE:1431656"
 /clone_lib="Sugano mouse liver mla"
 /sex="female"
 /dev_stage="adult"
 /lab_host="DH10B"
 /note="Organ: liver. Vector: pME18S-FL3. Site_1: DraIII
 (CACTGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA
 was primed with an oligo(dT) primer
 [ATGTGGCCCTTTTCTTTTCTT]; double-stranded cDNA was
 ligated to a DraIII adaptor [TGTGGCCCTACTGG], digested
 and cloned into distinct DraIII sites of the pME18S-FL3
 vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
 be used to isolate the cDNA insert. Size selection was
 performed to exclude fragments <1.5kb. Library
 constructed by Dr. Sumio Sugano (University of Tokyo
 Institute of Medical Science). Custom primers for
 sequencing: 5' end primer CTCTGCTCTAAAGCTGCG and 3' end
 primer CGACTGCGACTGACGACACA."
 BASE COUNT 109 a 95 c 126 g 98 t
 ORIGIN
 Query Match 1.8%; Score 20; DB 9; Length 428;
 Best Local Similarity 100.0%; Pred. No. 24;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 938 tgggctcaccctgatgttc 957
 |||||||
 Db 363 TGGGCTTCACCCCTGATGTTC 344
